

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 8, 2002, 15:40:22 ; Search time 25 Seconds

(without alignments)
2484.207 Million cell updates/sec

Title: US-09-744-748-1

Perfect score: 1770

Sequence: 1 MTSTSGKILRPLIVCIILG.....HVKRHOYKSVGNLEKFWFN 359

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SPREMBL_19.*
- 2: sp_archaea.*
- 3: sp_bacteria.*
- 4: sp_fungi.*
- 5: sp_human.*
- 6: sp_invertebrate.*
- 7: sp_mammal.*
- 8: sp_mhc.*
- 9: sp_organelle.*
- 10: sp_phage.*
- 11: sp_plant.*
- 12: sp_rodent.*
- 13: sp_virus.*
- 14: sp_vertebrate.*
- 15: sp_unclassified.*
- 16: sp_virus.*
- 17: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1970	100.0	359	11	O88819 mus musculus
2	1961	99.5	359	4	Q9Y231 homo sapien
3	1956	99.3	359	11	Q9JIG1 cricetus
4	1955	99.2	359	11	Q9JJB3 rattus norv
5	908.5	46.1	391	13	Q9W640 brachydanio
6	839	42.6	392	13	Q9W641 gallus gall
7	791	40.2	356	13	Q98952 rattus norv
8	704.5	35.8	433	11	Q9N888 cricetus
9	696	35.3	362	11	Q9R220 cricetus
10	694	35.2	362	11	Q9R219 cricetus
11	693	35.2	401	11	Q9JIK2 cricetus
12	689	35.0	362	11	Q95886 cricetus
13	688.5	34.9	386	11	Q920V9 mus musculus
14	688	34.9	390	11	Q920W0 mus musculus
15	687	34.9	390	11	Q920W1 mus musculus
16	687	34.9	390	11	Q920V7 mus musculus

17	687	34.9	390	11	Q91VB5	Q91vb5 mus musculus
18	687	34.9	390	11	Q91V20	Q91v20 mus musculus
19	686	34.8	390	11	Q920V6	Q920v6 mus spicile
20	683	34.7	390	11	Q920V8	Q920v8 mus musculus
21	672	34.1	360	6	Q9XT34	Q9xt34 sus scrofa
22	670	34.0	361	4	Q9PLW6	Q9plw6 homo sapien
23	667.5	33.9	359	4	Q9UND8	Q9und8 homo sapien
24	664.5	33.7	359	6	Q9GKU6	Q9gku6 pongo pygma
25	657	33.4	365	6	Q9TQQ3	Q9tqq3 bos taurus
26	582	29.5	351	5	Q76204	Q76204 schistosoma
27	387	19.6	426	5	Q9WJ24	Q9wj24 schistosoma
28	314	15.9	400	5	Q01906	Q01906 caenorhabdi
29	304	15.4	1652	5	Q22202	Q22202 caenorhabdi
30	302	15.3	312	5	Q9NSH5	Q9nsh5 caenorhabdi
31	285.5	14.5	451	5	Q21362	Q21362 caenorhabdi
32	258	13.1	489	11	Q9CXS9	Q9cxs9 mus musculus
33	235.5	12.0	405	10	Q93X61	Q93x61 beta vulgar
34	222	11.3	268	10	Q93WR9	Q93wr9 medicago tr
35	201	10.2	219	10	Q93WS0	Q93ws0 medicago tr
36	197	10.0	510	10	Q9ST51	Q9st51 phaseolus a
37	191.5	9.7	445	5	Q9W0F6	Q9w0f6 drosophila
38	170.5	8.7	292	5	Q76544	Q76544 dictyostell
39	157	8.0	475	2	Q9L8S4	Q9l8s4 helicobacte
40	156.5	7.9	183	16	Q92GR3	Q92gr3 rickettsia
41	156.5	7.9	338	2	O87135	O87135 vibrio chol
42	154.5	7.8	346	2	O87156	O87156 vibrio chol
43	153.5	7.8	338	2	O34231	O34231 vibrio chol
44	145	7.4	478	2	O30511	O30511 helicobacte
45	140.5	7.1	333	2	O32631	O32631 helicobacte

ALIGNMENTS

RESULT 1

ID	O88819	PRELIMINARY;	PRT;	359 AA.
AC	O88819;			
DT	01-NOV-1998 (TREMBLrel. 08, Created)			
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)			
DE	ALPHA-(1,3)-FUCOSYLTRANSFERASE (EC 2.4.1.-) (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE) (FUCOSYLTRANSFERASE 9) (FUCT-IX) (MFUC-TIX).			
GN	FUT9.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.			
RC	STRAIN=BALB/C; TISSUE=BRAIN;			
RX	MEDLINE=98434588; PubMed=9756916;			
RA	Kudo T., Ikehara Y., Togayachi A., Kaneko M., Hiraga T., Sasaki K.,			
RA	Narimatsu H.;			
RT	"Expression cloning and characterization of a novel murine alpha1, 3-			
RT	fucosyltransferase, mfuc-TIX, that synthesizes the Lewis x (CD15)			
RT	epitope in brain and kidney."			
RL	J. Biol. Chem. 273:26729-26738(1998).			
CC	-1- FUNCTION: MAY CATALYZE ALPHA-1,3 GLYCOSIDIC LINKAGES INVOLVED IN			
CC	THE EXPRESSION OF LEWIS X AND LEWIS Y.			
CC	-1- CATALYTIC ACTIVITY: GDP-L-FUCOSE + 1,4-BETA-D-GALACTOSYL-N-			
CC	ACETYL-D-GLUCOSAMINYL-R = GDP + 1,4-BETA-D-GALACTOSYL-(ALPHA-			
CC	1,3-L-FUCOSYL)-N-ACETYL-D-GLUCOSAMINYL-R.			
CC	-1- PATHWAY: GLYCOSYLATION.			
CC	-1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND			
CC	FORM IN TRANS CISTERNAE OF GOLGI.			
CC	-1- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN BRAIN AND KIDNEY. IT			
CC	ALSO EXPRESSED IN THE STOMACH, COLON, UTERUS AND EPIDIDYMIS. NOT			
CC	FOUND IN THYMUS, LIVER, SPLEEN, Ovary, LUNG, HEART, TESTIS AND			
CC	SMALL INTESTINE.			
DR	EMBL: AB015426; BAA33522.1; -			
DR	MGI: MGI:1330859; Fut9.			
DR	InterPro: IPR001503; Glyco_transf_10.			

DR	PFam: PF00852; Glyco_transf_10; 1.	
KW	Transferase; Glycosyltransferase; Transmembrane; Glycoprotein;	
KW	Signal-anchor; Golgi stack.	
DOMAIN	1 11	CYTOPLASMIC (POTENTIAL).
FT	1	SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT	12 30	(POTENTIAL).
FT	31 359	LOMENAL, CATALYTIC (POTENTIAL).
FT	CARBOHYD 62	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 101	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 153	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 153	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	SEQUENCE 359 AA; 42041 MW; 96A2394547F2A44E CRC64;	
FT	SEQUENCE 359 AA; 42041 MW; 96A2394547F2A44E CRC64;	
Query Match	100.0%; Score 1970; DB 11; Length 359;	
Best Local Similarity	100.0%; Pred. No. 1.le-142;	
Matches 359; Conservative	0; Mismatches 0; Indels 0; Gaps	
QY	1	MTSTSGILRFLPLVLCILGCFNACLLIYIKPTNSWVSPMESASSVLKMKNFSTKTDY 60
Db	1	MTSTSGILRFLPLVLCILGCFNACLLIYIKPTNSWVSPMESASSVLKMKNFSTKTDY 60
QY	61	FNETILVWVWVPGQTDLTSCAMENIOGCHLTITDRSLYNKSHAVLIHHRDLSWDTNL 120
Db	61	FNETILVWVWVPGQTDLTSCAMENIOGCHLTITDRSLYNKSHAVLIHHRDLSWDTNL 120
QY	121	POQARPPQKVIWNLESPTHPTOKSGIEHLNLTITRRSDLOVYGLTVSTNPFFV 180
Db	121	POQARPPQKVIWNLESPTHPTOKSGIEHLNLTITRRSDLOVYGLTVSTNPFFV 180
QY	181	EYVPSKEKLVCVWNNWPEHARVKKYINELSKSIEHTTGQAFGEYVNDKMLIPTISTCKP 240
Db	181	EYVPSKEKLVCVWNNWPEHARVKKYINELSKSIEHTTGQAFGEYVNDKMLIPTISTCKP 240
QY	241	YLUSFNSIHKDYITEKLYNAFLAGSVVVLGSPRENYENIYPADSFIHVEDFNPSSELAK 300
Db	241	YLUSFNSIHKDYITEKLYNAFLAGSVVVLGSPRENYENIYPADSFIHVEDFNPSSELAK 300
QY	301	YLKEVDKNNKLYLYSFYFNWRKDFVTNLPWFESHACIADCHVKRQEKYSVGNLEKFWFN 359
Db	301	YLKEVDKNNKLYLYSFYFNWRKDFVTNLPWFESHACIADCHVKRQEKYSVGNLEKFWFN 359
RESULT 2		
QYV231		
ID	Q9Y231	PRELIMINARY; PRT; 359 AA.
AC	Q9Y231;	
DT	01-NOV-1999 (TrEMBLrel. 12, Created)	
DT	01-NOV-1999 (TrEMBLrel. 12, Last sequence update)	
DT	01-JUN-2001 (TrEMBLrel. 17, Last annotation update)	
DE	ALPHA-3-FUCOSYLTRANSFERASE.	
DE	FUT9.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
OC	NCBI_Taxid=9606;	
RN	[1]	
RN	SEQUENCE FROM N.A.	
RC	TISSUE-WHOLE EMBRYO;	
RA	Caillaue A., Coullin P., Candeller J.J., Balanzino L., Oriol R.,	
RA	Mollicone R.;	
RT	"Cloning, expression and chromosome localization of a human embryonic	
RT	Fu9 transcript.";	
RL	Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.	
RL	[2]	
RL	SEQUENCE FROM N.A.	
RL	MEDLINE=99332063; PubMed=10405152;	
RX	Kaneko M., Kudo T., Iwasaki H., Ikehara Y., Nishihara S., Nakagawa S.,	
RA	Sasaki K., Shima T., Inoko N., Saitou N., Narimatsu H.;	
RT	"Human hepatitis B virus mutants: significance of molecular changes."	
RT	FEBS Lett. 453:237-242(1999).	
DR	EMBL; AJ238701; CAB41890.1; -	
DR	EMBL; AB023021; BAA81685.1; -	
DR	InterPro: IPR001503; Glyco_transf.10.	
DR	PFam: PF00852; Glyco_transf_10; 1.	

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FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 359 AA; 42071 MW; 9D5CD8BFF07EA902 CRC64;

Query Match 99.3%; Score 1956; DB 11; Length 359;
Best Local Similarity 98.9%; Pred. No. 1.3e-141;
Matches 355; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTSTSGILRPFLIVCIILGCFMACLLIYIKPTNSWVSPMESASSVLKMKNFSTKTDY 60
DQ 1 MTSTSGILRPFLIVCIILGCFMACLLIYIKPTNSWVSPMESASSVLKMKNFSTKTDY 60
QY 61 FNETTILVWVWPGQTFDLTSCQAMENIQGCHLTTRDSLYNKSHAVLIHHRDISWDLTNL 120
DQ 61 FNETTILVWVWPGQTFDLTSCQAMENIQGCHLTTRDSLYNKSHAVLIHHRDISWDLTNL 120
QY 121 PQOARPPQKWIWMNLESPHTPKQSGIEHLENLTITTYRRSDIQVPGFLTVSTNPFVF 180
DQ 121 PQOARPPQKWIWMNLESPHTPKQSGIEHLENLTITTYRRSDIQVPGFLTVSTNPFVF 180
QY 181 EVPSKEKLVWVYNNPNHARVYKYNELSKSIEIHTYGOAFGEYVNDKMLIPTISTCKF 240
DQ 181 EVPSKEKLVWVYNNPNHARVYKYNELSKSIEIHTYGOAFGEYVNDKMLIPTISTCKF 240
QY 241 YLSFENSIHKDYITEKLYNAFLAGSVVVLGSPRENYENIPADSFTHVEDFNSPSELAK 300
DQ 241 YLSFENSIHKDYITEKLYNAFLAGSVVVLGSPRENYENIPADSFTHVEDFNSPSELAK 300
QY 301 YLKEVDKNNKLYLSYFNWRKDFVNLPRFWEHSHACLDHVKRHOEYKSVGNLEKWFVN 359
DQ 301 YLKEVDKNNKLYLSYFNWRKDFVNLPRFWEHSHACLDHVKRHOEYKSVGNLEKWFVN 359

RESULT 4
Q99JB3 PRELIMINARY; PRT; 359 AA.
ID Q99JB3
AC Q99JB3
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE ALPHA1.3-FUCOSYLTRANSFERASE IX.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Shimoda Y., Tajima Y., Osanai T., Katsume A., Kohara M., Kudo T.,
RA Narimatsu H., Osumi N., Sanai Y.;
RT "Expression of Lewis x epitope in embryonic forebrain by regulating
RT alpha1,3-fucosyltransferase IX expression.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
[2]
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY;
RX MEDLINE=20472964; PubMed=11020213;
RA Baboval T., Henion T., Kinnally E., Smith F.I.;
RT "Molecular cloning of rat alpha1,3-fucosyltransferase IX and
RT comparison of the expression of fuc-TIV and fuc-TIX genes during rat
RT postnatal cerebellum development.";
RL J. Neurosci. Res. 62:206-215(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY;
RA Smith F.I., Baboval T.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049819; BAB40953.1; -.
DR EMBL; AF345993; AAK16591.1; -.
DR InterPro; IPR001503; Glyco_transf_10.
DR Pfam; PF00852; Glyco_transf_10; 1.
KW Transferase; Glycosyltransferase.
SQ SEQUENCE 359 AA; 42037 MW; 369B4A7BD0C6CC80 CRC64;

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Query Match 99.2%; Score 1955; DB 11; Length 359;
Best Local Similarity 99.2%; Pred. No. 1.6e-141;
Matches 356; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTSTSGILRPFLIVCIILGCFMACLLIYIKPTNSWVSPMESASSVLKMKNFSTKTDY 60
DQ 1 MTSTSGILRPFLIVCIILGCFMACLLIYIKPTNSWVSPMESASSVLKMKNFSTKTDY 60
QY 61 FNETTILVWVWPGQTFDLTSCQAMENIQGCHLTTRDSLYNKSHAVLIHHRDISWDLTNL 120
DQ 61 FNETTILVWVWPGQTFDLTSCQAMENIQGCHLTTRDSLYNKSHAVLIHHRDISWDLTNL 120
QY 121 PQOARPPQKWIWMNLESPHTPKQSGIEHLENLTITTYRRSDIQVPGFLTVSTNPFVF 180
DQ 121 PQOARPPQKWIWMNLESPHTPKQSGIEHLENLTITTYRRSDIQVPGFLTVSTNPFVF 180
QY 181 EVPSKEKLVWVYNNPNHARVYKYNELSKSIEIHTYGOAFGEYVNDKMLIPTISTCKF 240
DQ 181 EVPSKEKLVWVYNNPNHARVYKYNELSKSIEIHTYGOAFGEYVNDKMLIPTISTCKF 240
QY 241 YLSFENSIHKDYITEKLYNAFLAGSVVVLGSPRENYENIPADSFTHVEDFNSPSELAK 300
DQ 241 YLSFENSIHKDYITEKLYNAFLAGSVVVLGSPRENYENIPADSFTHVEDFNSPSELAK 300
QY 301 YLKEVDKNNKLYLSYFNWRKDFVNLPRFWEHSHACLDHVKRHOEYKSVGNLEKWFVN 359
DQ 301 YLKEVDKNNKLYLSYFNWRKDFVNLPRFWEHSHACLDHVKRHOEYKSVGNLEKWFVN 359

RESULT 5
Q9W640 PRELIMINARY; PRT; 391 AA.
ID Q9W640
AC Q9W640;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ALPHA(1.3)FUCOSYLTRANSFERASE.
GN FT1 OR ZFT1.
OS Brachydanio rerio (Zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Kageyama N., Natsuka S., Hase S.;
RT "Molecular cloning and characterization of two zebrafish
RT alpha(1.3)fucosyltransferase genes developmentally regulated in
RT embryogenesis.";
RL J. Biochem. 0:0-0(1999).
DR EMBL; AB023627; BAA76706.1; -.
DR ZFIN; ZDB-GENE-990715-17; ft1.
DR InterPro; IPR001503; Glyco_transf_10.
DR Pfam; PF00852; Glyco_transf_10; 1.
KW Transferase; Glycosyltransferase.
SQ SEQUENCE 391 AA; 45265 MW; 98826D0B3D9679C2 CRC64;

Query Match 46.1%; Score 908.5; DB 13; Length 391;
Best Local Similarity 45.5%; Pred. No. 1.4e-61;
Matches 178; Conservative 58; Mismatches 116; Indels 39; Gaps 6;

QY 1 MTSTSGILRPFLIVCIILGCFMACLLIYIKPTNSWVSP-----MESASSYLKM 50
DQ 6 LTPPSKA-AQKVIATFMILISFCIFPVYNNPTTFKFFPAVDVHTNCSTCTCLDLVK 64
QY 51 KNFST-----KTDYNETILVWVWPGQTFDLTSCQAMFNI 88
DQ 65 QNYKCTIKNASDNPSTPAPNPAPATAKDD--QETILLIWWYPPGAREDLGCGSQFNI 122
QY 89 QGCHLTDRSLYKSHAVLIHHRDISWDLTNLPPQARPPQKWIWMNLESPHTPKSGI 148
DQ 123 HGCHLTDRSLYKSHAVLIHHRDISWDLTNLPPQARPPQKWIWMNLESPHTPKSGI 179

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QY 149 EHLNLTJTYRRSDIOVPYGFLLTVSNPVP-FEVPSEKLVWVSNWNNPEHARVYKYN 207
DB 180 NDNGLNLTSSFKSDIPIVYGRLLDAYDEQKNFTIPKDKLVWVSNFQEHKRQSYNN 239
QY 208 ELKSIEIHTYGOAFGEYVNDKNLIPTISCKYLSFENSIRKDYITEKLYNAFLAGSVP 267
DB 240 ELVKHIVKVEAYGGHFNRRVDDYGNVSSCKFYLSFENSIRKDYITEKLYNAFLAGTVP 299
QY 268 VVLGSPRENYENYIPADSFHVEDFNSPSELAKYLKVDKNNKLYLSYFNWRKDFVNL 327
DB 300 VVLGSPRNDYEEFIPRDAFIHVDFFPKELADHLKSLDQNEQRYQYFNWRKHFISSMS 359
QY 328 RFWESHACLAGDVKHQRHGVKSVGNLSEKWF 358
DB 360 SFGLEHACRTCDYLKRNKHVIAITDLKGF 391

RESULT 6
Q9W641 PRELIMINARY; PRT; 392 AA.
AC Q9W641; 1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DE ALPHA(1,3)FUCOSYLTRANSFERASE.
GN FT2 OR ZFT2.
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Kageyama N., Natsuka S., Hase S.;
RT "Molecular cloning and characterization of two zebrafish
RT alpha(1,3)fucosyltransferase genes developmentally regulated in
RT embryogenesis.";
RL J. Biochem. 0:0-0(1999).
DR EMBL; AB023628; BAA76707.1; .
DR ZFIN; ZDB-GENE-990715-18; ft2.
DR InterPro; IPR001503; Glyco.transf.10.
DR Pfam; PF00852; Glyco.transf.10; 1.
KW Transferase; Glycosyltransferase.
SQ SEQUENCE 392 AA; 45944 MW; ABAC437E549C6114 CRC64;

Query Match 42.6%; Score 839; DB 13; Length 392;
Best Local Similarity 42.8%; Pred. No. 2,8e-56;
Matches 164; Conservative 61; Mismatches 122; Indels 36; Gaps 7;

QY 3 STSGILRPILVILVILGCPMACLL-IYKPTNSWFSP-----MESASSVLMK 51
DB 18 STQKLIVTFMLSLV-----CIFVYVNPNTFFKYPMTGMHANSSCSETCLHVKMQ 71
QY 52 NF-ESTTDYFN-----ETTILVWVWPGQTFDLTSCQAMPNIQGCCHLT 96
DB 72 NYECIMKASYNALPTPAPNAPKGDQDIIVLWMAFPVDFDLKDCGLEYNHGCQLYD 131
QY 97 RSLYNKSHAVLIHHRDISWDLNLPQOARPPFKQKWIWNLNLTPTQKSGIEHFNLT 156
DB 132 RSLQKAGVNFHHRDMS---TFDQPPDPDFQKWIWNLNLTPTQKSGIEHFNLT 188
QY 157 TYRSDSDIOVPYGFLLTVSNPVP-FEVPSEKLVWVSNWNNPEHARVYKYN 215
DB 189 SYNRSDSDIPYVGLVDATQEQKFTIPKDKLVWVSNFQEHKRQSYNN 248
QY 216 HTYGOAFGEYVNDKNLIPTISCKYLSFENSIRKDYITEKLYNAFLAGSVP 275
DB 249 STYGGHFNRRVDDYGNVSSCKFYLSFENSIRKDYITEKLYNAFLAGTVP 308
QY 276 NYENYIPADSFHVEDFNSPSELAKYLKVDKNNKLYLSYFNWRKDFVNL 335
DB 309 NYEFIPRDAFIHVDFFPKELADHLKSLDQNEQRYQYFNWRKHFISSMS 368

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QY 336 LACDVKHQRHGVKSVGNLEKWF 358
DB 369 RICDYLKRNKHVIAITDLKGF 391

RESULT 7
Q98952 PRELIMINARY; PRT; 356 AA.
AC Q98952;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DE ALPHA(1,3)-FUCOSYLTRANSFERASE (EC 2.4.1.7)
DE (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE) (FUCOSYLTRANSFERASE 4) (FUCT-IV)
DE (CTF1).
GN Gallus gallus (Chicken).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-97115837; PubMed-8955139;
RA Lee K.P., Carlson L.M., Woodcock J.B., Ramachandra N., Schultz T.L.,
RA Davis T.A., Lowe J.B., Thompson C.B., Larsen R.D.;
RL J. Biol. Chem. 271:32960-32967(1996).
CC -!- FUNCTION: MAY CATALYZE ALPHA-1,3 GLYCOSIDIC LINKAGES INVOLVED IN
CC THE EXPRESSION OF LEWIS X/SSEA-1 AND VIM-2 ANTIGENS.
CC -!- PATHWAY: GLYCOSYLATION.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC FORM IN TRANS CISTERNAE OF GOLGI.
CC -!- TISSUE SPECIFICITY: IN THE FOLLOWING EMBRYONIC TISSUES: BRAIN,
CC EYE, GIZZARD, THYMUS, BURSA AND SPLEEN.
CC EMBL; U73678; AAC60060.1; .
DR InterPro; IPR001503; Glyco.transf.10.
DR Pfam; PF00852; Glyco.transf.10; 1.
KW Transferase; Glycosyltransferase; Transmembrane; Glycoprotein;
KW Signal-anchor; Golgi stack.
FT DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 23 51 SIGNAL-ANCHOR
FT FT TYPE-II MEMBRANE PROTEIN.
FT LUMENAL, CATALYTIC (POTENTIAL).
FT N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 80 80 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 149 149 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 356 AA; 41494 MW; 13141627FEBAD089 CRC64;

Query Match 40.2%; Score 791; DB 13; Length 356;
Best Local Similarity 50.3%; Pred. No. 1,2e-52;
Matches 151; Conservative 49; Mismatches 94; Indels 6; Gaps 5;

QY 63 ETTILVWVWPGQTFDLTSCQAMPNIQGCCHLTTRSLYNKSHAVLIHHRDIS-WDLTNLP 121
DB 56 ETVTLVWVWPGQTFDLTSCQAMPNIQGCCHLTTRSLYNKSHAVLIHHRDIS-WDLTNLP 115
QY 122 Q--QARPPFQKWIWNLNLTPTQKSGIEHFNLTPTQKSGIEHFNLTPTQKSGIEHFNLTPT 179
DB 116 RGPPPPRPPRQVWVSNWNNPEHARVYKYNELKSIETHTYGOAFGEYVNDKNLIPTISCK 239
QY 180 FVLPSEKLVWVSNWNNPEHARVYKYNELKSIETHTYGOAFGEYVNDKNLIPTISCK 239
DB 176 FVLPSEKLVWVSNWNNPEHARVYKYNELKSIETHTYGOAFGEYVNDKNLIPTISCK 234
QY 240 FVLPSEKLVWVSNWNNPEHARVYKYNELKSIETHTYGOAFGEYVNDKNLIPTISCK 298
DB 235 FVLPSEKLVWVSNWNNPEHARVYKYNELKSIETHTYGOAFGEYVNDKNLIPTISCK 294
QY 299 AKYLEVDKNNKLYSYFNWRKDFVNLNPEWESHACLAGDVKHQRHGVKSVGNLEKWF 357
DB 295 ATYLAFLDKNKPYSRRYFAWRNKYEHVTSFWEHYCKVCEAVRTAGNQLTVQNLAGWF 354

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RESULT 8
Q99N88 PRELIMINARY; PRT; 433 AA.
AC Q99N88;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE ALPHA1,3-FUCOSYLTRANSFERASE.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Sanai Y., Shimoda Y., Tajima Y., Oosai T., Katsume A., Kohara M.,
RA Kudo T., Narimatsu H., Osumi N.;
RT "Expression of Lewis x epitope in embryonic forebrain.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049938; BAB40992.1; -.
DR InterPro; IPR001503; Glyco_transf_10.
DR Pfam; PF00852; Glyco_transf_10; 1.
KW Transferase; Glycosyltransferase.
SQ SEQUENCE 433 AA; 48918 MW; 1E1AFFB70EFA1402 CRC64;

Query Match 35.8%; Score 704.5; DB 11; Length 433;
Best Local Similarity 39.6%; Pred. No. 6e-46;
Matches 160; Conservative 51; Mismatches 118; Indels 75; Gaps 13;

QY 4 TSKGILRPFIVCIILGCFMACLLIYIKPTNSWVFSPMESASSVLKMKNFSTKTDYFNE 63
DB 53 TSSGLAAAGLL-CTAL---TACLWGQLPLPWA-SPAPO-----RP 89
QY 64 TTLVWVWF----GTFDLTSCQAMFNIQCHLTDRSLYNKSHAVLIHHRDI----- 113
DB 90 VSVLLMEPEGGRGHSGKPPDCSLRFTSGRCRLDRAAYGAQAQVLFHRLDVKGPPD 149
QY 114 ---SWDLTNLPOQA-----RPPFQKWIWNLESPTHTPOK 145
DB 150 WPPWGAQERTDALELRVFDDEGAVMLAREALETTGSRPPQQRVWMNFESPTHTPGL 209
QY 146 SGI-EHLNLTLYRRDSDIQVPGFLTVSTNPFVFPVS-----KEKLYCWVWSNW 196
DB 210 RGLAKDLFNWTLSTYRDSDFVPGFLYPRSH- -AEQPSGLPPLARKRLGLVAVVSHW 267
QY 197 NPEHARKVYNELSKSTEIHTYQCAF-GEYVNDKNLIPTISTCKFYLSPENSIHKDYITE 255
DB 268 NERQARYRYHQLRRHVSVDVFRAGPGQVPVAVGLLHTVARYKFKYLAFENSQHVYITE 327
QY 256 KLX-NAFLAGSVPVVLGSPSRENYENIPADSFTHVEDFNSPSELAKYLKEVDKNNKLYLS 314
DB 328 KLWRNFLAGVVPVLGPDVRANRYERFVRGSGFIHVDFFSAASLAAYLFLDRNAVYRR 387
QY 315 YFNWRKDTVNLPRFWESHACADCHKVHRH-QEYKSVGNLEKWF 357
DB 388 YFHWRSYAVHITSFWDPEPCQCRAVQTSQDQPKSIHNLADWF 431

RESULT 9
Q9R220 PRELIMINARY; PRT; 362 AA.
AC Q9R220;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE ALPHA (1,3) FUCOSYLTRANSFERASE 6A.
GN FUT6A.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.

Query Match 35.2%; Score 694; DB 11; Length 362;
Best Local Similarity 41.6%; Pred. No. 3e-45;
```

```
RX MEDLINE=99214609; PubMed=10187834;
RA Zhang A., Potvin B., Zaiman A., Chen W., Kumar R., Phillips L.,
RA Stanley P.;
RT "The gain-of-function chinese hamster ovary mutant LEC11B expresses
RT one of two chinese hamster FUT6 genes due to the loss of a negative
RT regulatory factor.";
RL J. Biol. Chem. 274:10439-10450(1999).
DR EMBL; AF090450; AAD24888.1; -.
DR InterPro; IPR001503; Glyco_transf_10.
DR Pfam; PF00852; Glyco_transf_10; 1.
KW Transferase; Glycosyltransferase.
SQ SEQUENCE 362 AA; 41767 MW; 2256EA145B03DA13 CRC64;

Query Match 35.3%; Score 696; DB 11; Length 362;
Best Local Similarity 41.6%; Pred. No. 2.1e-45;
Matches 149; Conservative 65; Mismatches 124; Indels 20; Gaps 10;

QY 10 RPFLIVCIILGCFMACLLIYIKPTNSWVFSPMESASSVLKMKNFSTKTDYF-NEETILV 68
DB 14 RPLGLILLQLLFCFFSIRVSHDQGPAPDSST-----GPASTPTTTPVPRPFLILL 68
QY 69 WVPFPGTQFDLTSCQAMF-NIOGCHLTDRSLYNKSHAVLIHHRDISWDLTN-LPQOARP 126
DB 69 WTPWFHSPLTLYPCSKMLPGTADQMTVNSLYPQADAVIFHHRDISPNRSLPSQRP 128
QY 127 PPKWTWNLSTHTPQKSGIEHLNLTLYRRDSDIQVPGFLTVSTNPFV---FEVP 183
DB 129 PGQWVWFSESPSHCSRLSALDGYFNLTMSYRSDSDIFTFYGNLEPWAEPVQTVNMS 188
QY 184 SKELKVCWVYNNPEHARKVYNELSKSTEIHTYQCAFGEYVNDKNLIPTISTCKFYL 243
DB 189 AKTDLVAVANNPNKSAVLYYQKLSQSHLDVYVGHGHP-LSRGDMGTLLARYKYLA 247
QY 244 FENSIHKDYITEKLY-NAFLAGSVPVVLGSPSRENYENIPADSFTHVEDFNSPSELAKYL 302
DB 248 FENSLHPDYITEKLNKNALEAWPVVLGSPSRKNYERFLPDFAFIHVDDESADLAQYL 307
QY 303 KEVDKNNKLYSFNWRKDTVNLPRFWESHA---CLACDHVKRHQYKSVGNLEKWF 357
DB 308 QKLDKDSQSYRFRWRETLR---PRL-SSMALAFCAQACRQLQWDRQYQTVHVSASF 361

RESULT 10
Q9R219 PRELIMINARY; PRT; 362 AA.
AC Q9R219;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ALPHA (1,3) FUCOSYLTRANSFERASE 6B.
GN FUT6B.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang A., Potvin B., Zaiman A., Chen W., Kumar R., Phillips L.,
RA Stanley P.;
RT "The gain-of-function chinese hamster ovary mutant LEC11B expresses
RT one of two chinese hamster FUT6 genes due to the loss of a negative
RT regulatory factor.";
RL J. Biol. Chem. 274:10439-10450(1999).
DR EMBL; AF090449; AAD24887.1; -.
DR InterPro; IPR001503; Glyco_transf_10.
DR Pfam; PF00852; Glyco_transf_10; 1.
KW Transferase; Glycosyltransferase.
SQ SEQUENCE 362 AA; 41743 MW; 480D106C40DE5F30 CRC64;

Query Match 35.2%; Score 694; DB 11; Length 362;
Best Local Similarity 41.6%; Pred. No. 3e-45;
```


GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 8, 2002, 15:40:22 ; Search time 25 Seconds
(without alignments)
2484.207 Million cell updates/sec

Title: US-09-744-748-2

Perfect score: 1970

Sequence: 1 WTSTSGILRPPLIVCIILG.....HVKRQEVKSVGNLEKFWN 359

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SPTEMBL19.*
- 2: sp_archaea.*
- 3: sp_bacteria.*
- 4: sp_fungi.*
- 5: sp_human.*
- 6: sp_invertebrate.*
- 7: sp_mammal.*
- 8: sp_mhc.*
- 9: sp_organelle.*
- 10: sp_phase.*
- 11: sp_plant.*
- 12: sp_rodent.*
- 13: sp_virus.*
- 14: sp_vertebrate.*
- 15: sp_unclassified.*
- 16: sp_rvirus.*
- 17: sp_bacteriap.*
- 18: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1970	100.0	359	4 Q9Y231	Q9Y231 homo sapien
2	1961	99.5	359	11 O88819	O88819 mus musculus
3	1954	99.2	359	11 Q9JIG1	Q9JIG1 cricetus
4	1946	98.8	359	11 Q9JTB3	Q9JTB3 rattus norv
5	906.5	46.0	391	13 Q9W640	Q9W640 brachydanio
6	837	42.5	392	13 Q9W641	Q9W641 gallus gall
7	792	40.2	356	13 Q9S952	Q9S952 rattus norv
8	700.5	35.6	433	11 Q9N888	Q9N888 rattus norv
9	692	35.1	362	11 Q9R220	Q9R220 cricetus
10	690	35.0	362	11 Q9R219	Q9R219 cricetus
11	690	35.0	401	11 Q9JIK2	Q9JIK2 cricetus
12	685.5	34.8	386	11 Q920V9	Q920V9 mus musculus
13	685	34.8	362	11 Q35886	Q35886 cricetus
14	684	34.8	390	11 Q920W0	Q920W0 mus musculus
15	684	34.7	390	11 Q920W1	Q920W1 mus musculus
16	684	34.7	390	11 Q920V7	Q920V7 mus musculus

17	684	34.7	390	11 Q91VB5	Q91VB5 mus musculus
18	684	34.7	390	11 Q91V20	Q91V20 mus musculus
19	683	34.7	390	11 Q920V6	Q920V6 mus spicile
20	680	34.5	390	11 Q920V8	Q920V8 mus musculus
21	669	34.0	360	6 Q9XT34	Q9XT34 sus scrofa
22	667	33.9	361	4 Q9PLW6	Q9PLW6 homo sapien
23	664.5	33.7	359	4 Q9UND8	Q9UND8 homo sapien
24	661.5	33.6	359	6 Q9GKU6	Q9GKU6 pongo pygma
25	653	33.1	365	6 Q9TQ03	Q9TQ03 bos taurus
26	579	29.4	351	5 Q76204	Q76204 schistosoma
27	383	19.4	426	5 Q9NJ24	Q9NJ24 schistosoma
28	318	16.1	400	5 Q01906	Q01906 caenorhabdi
29	308	15.6	1652	5 Q22202	Q22202 caenorhabdi
30	299	15.2	312	5 Q9NSH5	Q9NSH5 caenorhabdi
31	281.5	14.3	451	5 Q21362	Q21362 caenorhabdi
32	255	12.9	489	11 Q9CKS9	Q9CKS9 mus musculus
33	231.5	11.8	405	10 Q93X61	Q93X61 beta vulgar
34	219	11.1	268	10 Q93WR9	Q93WR9 medicago tr
35	200	10.2	219	10 Q93WS0	Q93WS0 medicago tr
36	196	9.9	510	10 Q9ST51	Q9ST51 phaseolus a
37	189.5	9.6	445	5 Q9W0F6	Q9W0F6 drosophila
38	170.5	8.7	292	5 Q76544	Q76544 dictyosteli
39	160.5	8.1	183	16 Q92GR3	Q92GR3 rickettsia
40	153.5	7.8	338	2 Q87135	Q87135 vibrio chol
41	153	7.8	475	2 Q9L8S4	Q9L8S4 helicobacte
42	151.5	7.7	346	2 Q87156	Q87156 vibrio chol
43	150.5	7.6	338	2 Q34231	Q34231 vibrio chol
44	142	7.2	478	2 Q30511	Q30511 helicobacte
45	137.5	7.0	333	2 Q32631	Q32631 helicobacte

ALIGNMENTS

RESULT 1

Q9Y231 ID Q9Y231 PRELIMINARY; PRT; 359 AA.
AC Q9Y231;
DT 01-NOV-1999 (TEMBLrel. 12, Created)
DT 01-NOV-1999 (TEMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE ALPHA-3-FUCOSYLTRANSFERASE.
GN FUT9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-WHOLE EMBRYO;
RA Caillieu A., Coullin P., Candellier J.J., Balanzino L., Oriol R.,
RA Mollicone R.;
RT "Cloning, expression and chromosome localization of a human embryonic
FUT9 transcript."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]

June 99.

Query Match 100.0%; Score 1970; DB 4; Length 359;
Best Local Similarity 100.0%; Pred. No. 6.8e-145;
Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
SQ SEQUENCE 359 AA; 42041 MW; C90CF5C02CB644D9 CRC64;

QY 1 MTSTSGKILRPLFLVCIILGCFMACLLIYIKPTNSWIFSPMESASSVLMKNFSTKTDY 60
 DB 1 MTSTSGKILRPLFLVCIILGCFMACLLIYIKPTNSWIFSPMESASSVLMKNFSTKTDY 60
 QY 61 FNETTILVWVWPFQGTDLTSCQAMFIQOCHLTDRSLYNKSHAVLIHHRDISWDLTNL 120
 DB 61 FNETTILVWVWPFQGTDLTSCQAMFIQOCHLTDRSLYNKSHAVLIHHRDISWDLTNL 120
 QY 121 PQOARPPQKWIWMNLESPTTPQKSGIEHLNLTLYRRSDIOVPYGLTSTNPFVF 180
 DB 121 PQOARPPQKWIWMNLESPTTPQKSGIEHLNLTLYRRSDIOVPYGLTSTNPFVF 180
 QY 181 EYPSKEKLVWVWVNNPEHARVYNNELSKSIEIHTYGOAFGEYVNDKNIPTISACKF 240
 DB 181 EYPSKEKLVWVWVNNPEHARVYNNELSKSIEIHTYGOAFGEYVNDKNIPTISACKF 240
 QY 241 YLSFNSIHKDYITEKLYNAFLAGSPVVLGSPRENYENIPADSFHVEDYNSPELAK 300
 DB 241 YLSFNSIHKDYITEKLYNAFLAGSPVVLGSPRENYENIPADSFHVEDYNSPELAK 300
 QY 301 YLKEVDKNNKLYLSYFNWRKDFTNLPRFWESHACLDHVHRQEKYSVGNLEKFWFN 359
 DB 301 YLKEVDKNNKLYLSYFNWRKDFTNLPRFWESHACLDHVHRQEKYSVGNLEKFWFN 359

RESULT 2
 O88819 ID O88819 PRELIMINARY: PRT: 359 AA.
 AC O88819;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE ALPHA-(1,3)-FUCOSYLTRANSFERASE (EC 2.4.1.-) (GALACTOSIDE 3-L-
 FUCOSYLTRANSFERASE) (FUCOSYLTRANSFERASE 9) (FUCT-IX).
 GN FUT9.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
 RC STRAIN=BALE/C; TISSUE=BRAIN;
 RX MEDLINE=98434588; PubMed=9756916;
 RA Kudo T., Ikehara Y., Togayachi A., Kaneko M., Hiraga T., Sasaki K.,
 RA Narimatsu H.;
 RT "Expression cloning and characterization of a novel murine alphanal, 3-
 RT fucosyltransferase, mFuc-TIX, that synthesizes the Lewis x (CD15)
 RT epitope in brain and kidney."
 RL J. Biol. Chem. 273:26729-26738(1998).
 CC -!- FUNCTION: MAY CATALYZE ALPHA-1,3 GLYCOSIDIC LINKAGES INVOLVED IN
 CC THE EXPRESSION OF LEWIS X AND LEWIS Y.
 CC -!- CATALYTIC ACTIVITY: GDP-L-FUCOSE + 1,4-BETA-D-GALACTOSYL-N-
 CC ACETYL-D-GLUCOSAMINYL-R = GDP + 1,4-BETA-D-GALACTOSYL-(ALPHA-
 CC 1,3-L-FUCOSYL)-N-ACETYL-D-GLUCOSAMINYL-R.
 CC -!- PATHWAY: GLYCOSYLATION.
 CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
 CC FORM IN TRANS CISTERNAE OF GOLGI.
 CC -!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN BRAIN AND KIDNEY. IT
 CC ALSO EXPRESSED IN THE STOMACH, COLON, UTERUS AND EPIDIDYMIS. NOT
 CC FOUND IN THYMUS, LIVER, SPLEEN, OVARY, LUNG, HEART, TESTIS AND
 CC SMALL INTESTINE.
 DR EMBL; AB015426; BAA33522.1; -.
 DR MGB; MGI:1330859; Fuc9.
 DR InterPro; IPR001503; Glyco_transf_10.
 DR Pfam; PF00852; Glyco_transf_10; 1.
 KW Transferase; Glycosyltransferase; Transmembrane; Glycoprotein;
 KW Signal-anchor; Golgi stack.
 FT DOMAIN 1 11
 FT TRANSMEM 12 30
 FT SIGNAL-ANCHOR (POTENTIAL).
 FT CYTOPLASMIC (POTENTIAL).
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT LUMENAL, CATALYTIC (POTENTIAL).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 101 101

FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 359 AA; 42041 MW; 96A2394547F2A44E CRC64;
 Query Match 99.5%; Score 1961; DB 11; Length 359;
 Best Local Similarity 99.2%; Pred. No. 3.4e-144;
 Matches 356; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MTSTSGKILRPLFLVCIILGCFMACLLIYIKPTNSWIFSPMESASSVLMKNFSTKTDY 60
 DB 1 MTSTSGKILRPLFLVCIILGCFMACLLIYIKPTNSWIFSPMESASSVLMKNFSTKTDY 60
 QY 61 FNETTILVWVWPFQGTDLTSCQAMFIQOCHLTDRSLYNKSHAVLIHHRDISWDLTNL 120
 DB 61 FNETTILVWVWPFQGTDLTSCQAMFIQOCHLTDRSLYNKSHAVLIHHRDISWDLTNL 120
 QY 121 PQOARPPQKWIWMNLESPTTPQKSGIEHLNLTLYRRSDIOVPYGLTSTNPFVF 180
 DB 121 PQOARPPQKWIWMNLESPTTPQKSGIEHLNLTLYRRSDIOVPYGLTSTNPFVF 180
 QY 181 EYPSKEKLVWVWVNNPEHARVYNNELSKSIEIHTYGOAFGEYVNDKNIPTISACKF 240
 DB 181 EYPSKEKLVWVWVNNPEHARVYNNELSKSIEIHTYGOAFGEYVNDKNIPTISACKF 240
 QY 241 YLSFNSIHKDYITEKLYNAFLAGSPVVLGSPRENYENIPADSFHVEDYNSPELAK 300
 DB 241 YLSFNSIHKDYITEKLYNAFLAGSPVVLGSPRENYENIPADSFHVEDYNSPELAK 300
 QY 301 YLKEVDKNNKLYLSYFNWRKDFTNLPRFWESHACLDHVHRQEKYSVGNLEKFWFN 359
 DB 301 YLKEVDKNNKLYLSYFNWRKDFTNLPRFWESHACLDHVHRQEKYSVGNLEKFWFN 359

RESULT 3
 O88819 ID O88819 PRELIMINARY: PRT: 359 AA.
 AC O88819;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE ALPHA-(1,3)-FUCOSYLTRANSFERASE (EC 2.4.1.-) (GALACTOSIDE 3-L-
 DE FUCOSYLTRANSFERASE) (FUCOSYLTRANSFERASE 9) (FUCT-IX).
 GN FUT9.
 OS Cricetus griseus (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Cricetulus.
 OX NCBI_TaxID=10029;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=OVARY;
 RX MEDLINE=20165953; PubMed=10700388;
 RA Patnaik S.K., Zhang A., Shi S., Stanley P.;
 RA "Alpha(1,3)fucosyltransferases expressed by the gain-of-function
 RT Chinese hamster ovary glycosylation mutants LEC12, LEC29, and LEC30."
 RL Arch. Biochem. Biophys. 375:322-332(2000).
 CC -!- FUNCTION: MAY CATALYZE ALPHA-1,3 GLYCOSIDIC LINKAGES INVOLVED IN
 CC THE EXPRESSION OF LEWIS X AND LEWIS Y.
 CC -!- CATALYTIC ACTIVITY: GDP-L-FUCOSE + 1,4-BETA-D-GALACTOSYL-N-
 CC ACETYL-D-GLUCOSAMINYL-R = GDP + 1,4-BETA-D-GALACTOSYL-(ALPHA-
 CC 1,3-L-FUCOSYL)-N-ACETYL-D-GLUCOSAMINYL-R.
 CC -!- PATHWAY: GLYCOSYLATION.
 CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
 CC FORM IN TRANS CISTERNAE OF GOLGI.
 DR EMBL; AF230460; AAF82412.1; -.
 DR InterPro; IPR001503; Glyco_transf_10.
 DR Pfam; PF00852; Glyco_transf_10; 1.
 KW Transferase; Glycosyltransferase; Transmembrane; Glycoprotein;
 KW Signal-anchor; Golgi stack.
 FT DOMAIN 1 11
 FT TRANSMEM 12 30
 FT SIGNAL-ANCHOR (POTENTIAL).
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT LUMENAL, CATALYTIC (POTENTIAL).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 62 62

FT CARBOHYD 101 101 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 153 153 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 359 AA; 42071 MW; 95CD8BFF07EA902 CRC64;

Query Match 99.2%; Score 1954; DB 11; Length 359;
 Best Local Similarity 98.6%; Pred. No. 1.2e-143;
 Matches 354; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTSTSGILRPFLIVCIILGCFMACLLIYIKPTNSWIFSPMESASSVLMKKNFFSTKTDY 60
 DB 1 MTSTSGILRPFLIVCIILGCFMACLLIYIKPTNSWIFSPMESASSVLMKKNFFSTKTDY 60
 QY 61 FNETTILVWVWPGQTFDLTSCQAMFNIQCHLTTRDSLYNKSHAVLIHHRDISWDLTNL 120
 DB 61 FNETTILVWVWPGQTFDLTSCQAMFNIQCHLTTRDSLYNKSHAVLIHHRDISWDLTNL 120
 QY 121 PQOARPPFKIWMNLESPTHTPKSGIEHLNLTLYRRSDIQVPGFLTVSTNPFV 180
 DB 121 PQOARPPFKIWMNLESPTHTPKSGIEHLNLTLYRRSDIQVPGFLTVSTNPFV 180
 QY 181 EVPSKEKLVGVVSNWNNPEHARVYKYNELSKSIEIHTYGOAFGEYVNDKNIPTISACKF 240
 DB 181 EVPSKEKLVGVVSNWNNPEHARVYKYNELSKSIEIHTYGOAFGEYVNDKNIPTISACKF 240
 QY 241 YLSPFENIHKDYITEKLYNAGVLAGSVPVLGSPRENYENIPADSFTHVEDYNSPSELAK 300
 DB 241 YLSPFENIHKDYITEKLYNAGVLAGSVPVLGSPRENYENIPADSFTHVEDYNSPSELAK 300
 QY 301 YLKEVDKNNKLYLSYFNWRKDFTVNLPWFESHACIADCHVHRHQEKYSVGNLEKWFVN 359
 DB 301 YLKEVDKNNKLYLSYFNWRKDFTVNLPWFESHACIADCHVHRHQEKYSVGNLEKWFVN 359

RESULT 4
 Q99JB3 PRELIMINARY; PRT; 359 AA.

ID Q99JB3
 AC Q99JB3
 DT 01-JUN-2001 (T-EMBLrel. 17, Created)
 DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
 DE ALPHA1,3-FUCOSYLTRANSFERASE IX.
 GN FUT9.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shimoda Y., Tajima Y., Osanai T., Katsume A., Kohara M., Kudo T.,
 RA Narimatsu H., Osumi N., Sanai Y.;
 RT "Expression of Lewis x epitope in embryonic forebrain by regulating
 RT alpha1,3-fucosyltransferase IX expression.";
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY;
 RX MEDLINE=20472964; PubMed=11020213;
 RA Baboval T., Henion T., Kinnally E., Smith F.I.;
 RT "Molecular cloning of rat alpha1,3-fucosyltransferase IX (Fuc-TIX) and
 RT comparison of the expression of fuc-TIV and fuc-TIX genes during rat
 RT postnatal cerebellum development.";
 RL J. Neurosci. Res. 62:206-215(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY;
 RA Smith F.I., Baboval T.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB049819; BAB40953.1; -;
 DR EMBL; AF345993; AAK16591.1; -;
 DR InterPro; IPR001503; Glyco_transf_10.
 DR Pfam; PF00852; Glyco_transf_10; 1.
 KW Transferase; Glycosyltransferase.
 SQ SEQUENCE 359 AA; 42037 MW; 36984A7BD0C6CC80 CRC64;

Query Match 98.8%; Score 1946; DB 11; Length 359;
 Best Local Similarity 98.3%; Pred. No. 4.9e-143;
 Matches 353; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTSTSGILRPFLIVCIILGCFMACLLIYIKPTNSWIFSPMESASSVLMKKNFFSTKTDY 60
 DB 1 MTSTSGILRPFLIVCIILGCFMACLLIYIKPTNSWIFSPMESASSVLMKKNFFSTKTDY 60
 QY 61 FNETTILVWVWPGQTFDLTSCQAMFNIQCHLTTRDSLYNKSHAVLIHHRDISWDLTNL 120
 DB 61 FNETTILVWVWPGQTFDLTSCQAMFNIQCHLTTRDSLYNKSHAVLIHHRDISWDLTNL 120
 QY 121 PQOARPPFKIWMNLESPTHTPKSGIEHLNLTLYRRSDIQVPGFLTVSTNPFV 180
 DB 121 PQOARPPFKIWMNLESPTHTPKSGIEHLNLTLYRRSDIQVPGFLTVSTNPFV 180
 QY 181 EVPSKEKLVGVVSNWNNPEHARVYKYNELSKSIEIHTYGOAFGEYVNDKNIPTISACKF 240
 DB 181 EVPSKEKLVGVVSNWNNPEHARVYKYNELSKSIEIHTYGOAFGEYVNDKNIPTISACKF 240
 QY 241 YLSPFENIHKDYITEKLYNAGVLAGSVPVLGSPRENYENIPADSFTHVEDYNSPSELAK 300
 DB 241 YLSPFENIHKDYITEKLYNAGVLAGSVPVLGSPRENYENIPADSFTHVEDYNSPSELAK 300
 QY 301 YLKEVDKNNKLYLSYFNWRKDFTVNLPWFESHACIADCHVHRHQEKYSVGNLEKWFVN 359
 DB 301 YLKEVDKNNKLYLSYFNWRKDFTVNLPWFESHACIADCHVHRHQEKYSVGNLEKWFVN 359

RESULT 5
 Q9W640 PRELIMINARY; PRT; 391 AA.

ID Q9W640
 AC Q9W640
 DT 01-NOV-1999 (T-EMBLrel. 12, Created)
 DT 01-NOV-1999 (T-EMBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
 DE ALPHA(1,3)-FUCOSYLTRANSFERASE.
 GN FT1 OR ZFT1.
 OS Brachydanio rerio (Zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kageyama N., Natsuka S., Hase S.;
 RT "Molecular cloning and characterization of two zebrafish
 RT alpha(1,3)-fucosyltransferase genes developmentally regulated in
 RT embryogenesis.";
 RL J. Biochem. 0:0-0(1999).
 DR EMBL; AB023627; BAA76706.1; -;
 DR ZFIN; ZDB-GENE-990715-17; ft1.
 DR InterPro; IPR001503; Glyco_transf_10.
 DR Pfam; PF00852; Glyco_transf_10; 1.
 KW Transferase; Glycosyltransferase.
 SQ SEQUENCE 391 AA; 45265 MW; 98826D0B3D9679C2 CRC64;

Query Match 46.0%; Score 906.5; DB 13; Length 391;
 Best Local Similarity 45.3%; Pred. No. 2e-62;
 Matches 177; Conservative 59; Mismatches 116; Indels 39; Gaps 6;

QY 1 MTSTSGILRPFLIVCIILGCFMACLLIYIKPTNSWIFSP-----MESASSVLMK 50
 DB 6 LTPPSKA-AQKVIATMELISFVCIFFVYVNPNTTFKFFPAVDVHTNCSTCTCLDVLKK 64
 QY 51 KNFST-----KTDYFNETTILVWVWPGQTFDLTSCQAMFNI 88
 DB 65 QNYKCTIKNASDNPSTTAPNAPATAKDD--QETILLIIVYFPGAREDLGCGSOFNI 122
 QY 89 QGCHLTTRDSLYNKSHAVLIHHRDISWDLTNLQQARPPFKIWMNLESPTHTPKSGI 148
 DB 123 HGCHLTTRDSLYNKSHAVLIHHRDISWDLTNLQQARPPFKIWMNLESPTHTPKSGI 179

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QY 149 EHLNLTITLRDSDIQPYGLFVSTNPFV-FEYPSKEKLVGVVSNWNEPHARVKYIN 207
Db 180 NDCGNLTSTFRSDSDIPYVGRLLDADQKNFTIPKDKLVGVVSNFQHHKRSYIN 239
QY 208 ELKSIEIHTYGOAFGEVYVNDKNLIPTISACKFYLSPENSITHKDYITEKLYNAPLAGSV 267
Db 240 ELVRHKIKVEAYGGHFNVRNDDYGVNVSSCKFYLSPENSITHRDYFTEKLFNPLAGTVP 299
QY 268 VVLGSPRENYENYIPADSFIVHEDYNSPSELAKYLKVDKNNKLYLSYFNWRKDFVTNLP 327
Db 300 VVLGSPRENYEYIPADSFIVHEDYNSPSELAKYLKVDKNNKLYLSYFNWRKDFVTNLP 359
QY 328 RWESHACLADHVHRKHQYKSVGNLEKWF 358
Db 360 SGLEHACRTCDYLKRNKHIAIKDLKGF 390

RESULT 6
Q9W641 PRELIMINARY; PRT; 392 AA.
AC Q9W641;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE ALPHA(1,3)FUCOSYLTRANSFERASE.
GN FT2 OR ZFT2.
OS Brachydanio rerio (zebrafish) (Zebra daniel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Kageyama N., Natsuka S., Hase S.;
RT "Molecular cloning and characterization of two zebrafish
RT alpha(1,3)fucosyltransferase genes developmentally regulated in
RT embryogenesis.";
RL J. Biochem. 0:0-(1999).
DR EMBL; AB023628; BAA76707.1; .
DR ZFIN; ZDB-GENE-990715-18; ft2.
DR InterPro; IPR001503; Glyco.transf.10.
DR Pfam; PF00852; Glyco.transf.10.1.
KW Transferase; Glycosyltransferase.
SQ SEQUENCE 392 AA; 45944 MW; ABAC437B549C6114 CRC64;

Query Match 42.5%; Score 837; DB 13; Length 392;
Best Local Similarity 42.6%; Pred. No. 4.9e-57;
Matches 163; Conservative 62; Mismatches 122; Indels 36; Gaps 7;

QY 3 STSGILRPPLIVCIILGCFMACLL-IYIKPTNSWIFSP-----MESASSVLKMK 51
Db 18 STQKLIVTFMLISLV-----CIFYYVNPNTFFKYPMTGTHANSSCSETCLHLKMQ 71
QY 52 NF-FSTKTDYFN-----ETTLVWVWPFQTFDLTSCQAMFNIQGCCHLT 96
Db 72 NYECIMKNASYNALPTPAPNPAKGDODIILVIMAPPFVFDLDCGLEYNHGCQLTYD 131
QY 97 RSLYNKSHAVLIHRDLSWDLNLPQOARPPFQKWIIMNLESPTHTPOKSGIEHFNLT 156
Db 132 RSLIQKAGVNFHHRDMS---TDFPQPPDFQKWIIMNLESPTHTPOKSGIEHFNLT 198
QY 157 TYRSDSDIQVPGFLTYST-NPFVFEVPSKEKLVGVVSNWNEPHARVKYINLSKIEI 215
Db 189 SYNRSDDIPVYGRVLDATTEQKFTIPKDKLVGVVSNFQHHKRSYIN 248
QY 216 HTYGOAFGEVYVNDKNLIPTISACKFYLSPENSITHKDYITEKLYNAPLAGSV 275
Db 249 STYGGHFNRRINGDDYGVNVSSCKFYLSPENSITHRDYFTEKLFNPLAGTVP 308
QY 276 NYENYIPADSFIVHEDYNSPSELAKYLKVDKNNKLYLSYFNWRKDFVTNLP 335
Db 309 NYEYIPADSFIVHEDYNSPSELAKYLKVDKNNKLYLSYFNWRKDFVTNLP 368
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QY 336 LACDHVHRKHQYKSVGNLEKWF 358
Db 369 RICDYLKRNKHIAVTDLKGF 391

RESULT 7
Q98952 PRELIMINARY; PRT; 356 AA.
AC Q98952;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE ALPHA-(1,3)-FUCOSYLTRANSFERASE (EC 2.4.1.-)
DE (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE) (FUCOSYLTRANSFERASE 4) (FUCT-IV)
DE (CTF1).
GN Cpt1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-97115837; PubMed-8955139;
RA Lee K.P., Carlson L.M., Woodcock J.B., Ramachandra N., Schultz T.L.,
RA Davis T.A., Lowe J.B., Thompson C.B., Larsen R.D.;
RL J. Biol. Chem. 271:32960-32967(1996).
CC -!- FUNCTION: MAY CATALYSE ALPHA-1,3 GLYCOSIDIC LINKAGES INVOLVED IN
CC THE EXPRESSION OF LEWIS X/SSEA-1 AND VIM-2 ANTIGENS.
CC -!- PATHWAY: GLYCOSYLATION.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC FORM IN TRANS CISTERNAE OF GOLGI.
CC -!- TISSUE SPECIFICITY: IN THE FOLLOWING EMBRYONIC TISSUES: BRAIN,
CC EYE, GIZZARD, THYMUS, BURSA AND SPLEEN.
DR EMBL; U73678; AAC60060.1; .
DR InterPro; IPR001503; Glyco.transf.10.
DR Pfam; PF00852; Glyco.transf.10.1.
KW Transferase; Glycosyltransferase; Transmembrane; Glycoprotein;
KW Signal anchor; Golgi stack.
FT DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 23 51 SIGNAL-ANCHOR
FT DOMAIN 52 356 (TYPE-II MEMBRANE PROTEIN).
FT CARBOHYD 80 80 LUMENAL, CATALYTIC (POTENTIAL).
FT CARBOHYD 149 149 N-LINKED (GLCNAC...) (POTENTIAL).
FT SEQUENCE 356 AA; 41494 MW; 13141627FEBAD089 CRC64;

Query Match 40.2%; Score 792; DB 13; Length 356;
Best Local Similarity 50.3%; Pred. No. 1.3e-53;
Matches 151; Conservative 50; Mismatches 93; Indels 6; Gaps 5;

QY 63 ETTILVWVWPFQTFDLTSCQAMFNIQGCCHLTDRSLYNKSHAVLIHRDLS-WDLNLP 121
Db 56 ETVLLWVEPFGRPRKPADCRRRYNTGCLLSADRGRYGEARVLFHRDLALHGRQLP 115
QY 122 Q-QARPPFQKWIIMNLESPTHTPOKSGIEHFNLTLYRSDSDIQVPGFLTYSTNPFV 179
Db 116 RGPPPRPQRQVWVNFESPSHSPGLRGLAGLFWNTWYSRSDSVFVPGYLYEPSPRP 175
QY 180 FEVPSKEKLVGVVSNWNEPHARVKYINLSKIEIHTYGOAFGEVYVNDKNLIPTISACK 239
Db 176 FVLPRKSLVAVVSNWNEPHARVKYINLSKIEIHTYGOAFGEVYVNDKNLIPTISACK 234
QY 240 FYLSFENSITHKDYITEKLY-NAFLAGSVVVLGSPRENYENYIPADSFIVHEDYNSPSEL 298
Db 235 FYLAFENSITHKDYITEKLYNAFLAGSVVVLGSPRENYENYIPADSFIVHEDYNSPSEL 294
QY 299 AKYLEVDKNNKLYLSYFNWRKDFVTNLPFWESHACLDHVRK-RHOEYKSVGNLEKWF 357
Db 295 ATYLKFLDKNPKSYRRYFAWRNKYEVHVTFSWDEHYCKVCEAVRTAGNQLKTVONLAW 354
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Matches 148; Conservative 66; Mismatches 124; Indels 20; Gaps 10;

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QY 10 RPLVLCVLCACMACILLIYIKPNWIFSPMESASSVLKMKNFSTKDYF-NEITILV 68
DB 14 RPLGLGLLQALLFALCFESYIRVSDQGGPPADSSP-----GPASTPTTPVPRPLILL 68
QY 69 WVPDPGQTFDLTSCQAMP-NIOCHLTDRSLYNKSHAVLIHHRDISWDLTN-LPOQARP 126
DB 69 WTPFPSPPLTLYPCSKMLPGTACOMVNSLTPQADAVIFHREISLPNPSRLPSQRP 128
QY 127 PFQKIWMNLESPTHTPKQSGIEHFNLTLYTRDSDIQVPYGLFVSTNPFV---FEYP 183
DB 129 PGQRWVFSLESPSHCSRLSALDGHFNLTMSYRSDDFTTYPGWLEPWAEPVQTVQVNS 188
QY 184 SKEKLVCVVSNWNPHEHARVYKYNELSKSIEHTYKGARGEYVNDKNLPTISACKFYLS 243
DB 189 AKTDLVAVASVNNPKSARVLYYQKLSHLHVDYVGRGHP-LSRQDMGTGLARYKFYLA 247
QY 244 FENSIHKDYITEKLY-NAFLAGSVVPLVGLPSRENYENYIPADSFTHVEDYNSPSELAKYL 302
DB 248 FENSLHPDYITEKLYNALEAWAVPVVGLPSRKNYERFTLPDAFTHVDDFSPADLAQYL 307
QY 303 KEVDKNNKLYSFENRKRKDTVNLPRFESHA---CLACDHVKRHOEYKSVGNLEKWF 357
DB 308 QKLDKDSQSYQRYFRWRETILR---PRL-SSMALAFQACROLOWDORTQTVHVSASWF 361

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RESULT 11

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Q9JIK2
ID Q9JIK2 PRELIMINARY; PRT; 401 AA.
AC Q9JIK2
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE ALPH-1,3-FUCOSYLTRANSFERASE (EC 2.4.1.-) (GALACTOSIDE 3-L-
DE FUCOSYLTRANSFERASE) (FUCOSYLTRANSFERASE 4) (FUCT-IV).
GN FUCT4.
OS Mus musculus (House mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mus.
OX NCBI-TaxID=10029;
RN 111-TaxID=10029;
RP SEQUENCE FROM N.A.
RC TISSUE-Ovary.
RX MEDLINE=20166953; PubMed=10700389;
RA Patnaik S.K., Zhang A., Shi S., Stanley P.;
RT "Alpha(1,3)-fucosyltransferases expressed by the gain-of-function
RT Chinese hamster ovary glycosylation mutants LEC12, LEC29, and LEC30.";
RL Arch. Biochem. Biophys. 375:322-332(2000).
CC 1- FUNCTION: MAY CATALYZE ALPHA-1,3 GLYCOSIDIC LINKAGES INVOLVED IN
CC THE EXPRESSION OF CELL SURFACE GLYCOPROTEINS AND LECTIN RECOGNITION.
CC 2- CATALYTIC ACTIVITY: GDP-L-FUCOSE + 1,4-BETA-D-GALACTOSYL-N-
CC ACETYL-D-GLUCOSAMINYL-R = GDP + 1,4-BETA-D-GALACTOSYL-(ALPHA-
CC 1,3-L-FUCOSYL)-N-ACETYL-D-GLUCOSAMINYL-R.
CC 3- PATHWAY: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC FORM IN TRANS CISTERNAE OF GOLGI.
CC 4- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 5- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 6- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 7- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 8- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 9- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 10- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 11- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 12- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 13- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 14- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 15- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 16- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 17- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 18- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 19- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 20- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 21- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 22- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 23- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 24- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 25- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 26- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 27- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 28- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 29- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 30- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 31- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 32- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 33- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 34- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 35- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 36- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 37- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 38- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 39- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 40- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 41- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 42- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 43- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 44- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 45- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 46- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 47- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 48- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 49- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 50- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 51- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 52- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 53- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 54- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 55- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 56- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 57- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 58- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 59- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 60- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 61- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 62- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 63- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 64- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 65- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 66- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 67- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 68- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 69- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 70- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 71- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 72- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 73- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 74- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 75- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 76- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 77- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 78- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 79- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 80- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 81- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 82- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 83- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 84- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 85- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 86- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 87- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 88- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 89- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 90- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 91- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 92- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 93- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 94- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 95- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 96- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 97- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 98- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 99- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC 100- FUNCTION: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND

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Query Match

Best Local Similarity 41.3%; Pred. No. 1.2e-45; Length 401;

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Matches 141; Conservative 54; Mismatches 96; Indels 50; Gaps 8;
QY 66 ILVAVWVWP-----GQTFDLTSCQAMFNIOGCHLTDRSLYNKSHAVLIHHRDISWDLTNLP 121
DB 60 VLLWVEPFGRGYKPPSPDCLRNISGCLLTDRAAYGEAQAVLFHHRDLVTGLSDWP 119
QY 122 QQ-----ARPPFKIWMNLESPTHTPKQSG 147
DB 130 PPWGAQVRDEALQRFVDDQEGNAMLAGEALETAGSRPPGQRWVWNNFSPSHSPLGLR 179
QY 148 I-EHLENLTLYTRDSDIQVPYGLFVSTNPFVFEVPS-----KEKLVCVVSNWNP 199
DB 180 LAKNLFNWTLSYRSDSVFVYGLFPLRSP-TCQPPGLSPPLARKRGLVAVVSWDER 238
QY 200 HARVYKYNELSKSIEHTYGO-AGGEVYVNDKNLPTISACKFYLSFENSIEHKDYITEKLY 258
DB 239 QARVYVYRQLIQHVVDVFGRAAVGKVPVPSGLLHVARYKFLAFENSQHVVDYITEKLY 298
QY 259 -NAFLAGSVVPLVGLPSRENYENYIPADSFTHVEDYNSPSELAKYLKEVDKNNKLYSYFN 317
DB 299 RNAFLAGAVPVVGLPDRANERFVPRGSFTHVDDFFSAASLAAYLLFLDRLNLAAYVRYPH 358
QY 318 WRKDFVNLPRFESHAACLDHVKRH-OEYKSVGNLEKWF 357
DB 359 WRRSYAVHITSFWDPEWCRTQCAVQTSQDPKSIQNLASWF 399

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RESULT 12

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Q920V9
ID Q920V9 PRELIMINARY; PRT; 386 AA.
AC Q920V9
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE ALPH-1,3-FUCOSYLTRANSFERASE (FRAGMENT).
GN FUCT4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI-TaxID=10090;
RN 111-TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN-BL/2/MSF;
RA Liu Y., Kitano T., Koide T., Shiroishi T., Moriaki K., Saitou N.;
RT "Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes of
RT Five Mus musculus subspecies.";
RL Submet. (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB039146; BAB68650.1; -.
KW Transferrase; Glycosyltransferase.
FT NON_TER 386
FT SEQUENCE 386 AA; 43812 MW; 6E057C1A29F99A70 CRC64;
Query Match
Best Local Similarity 34.8%; Score 685.5; DB 11; Length 386;
Matches 142; Conservative 47; Mismatches 86; Indels 47; Gaps 8;
QY 66 ILVAVWVWP-----GQTFDLTSCQAMFNIOGCHLTDRSLYNKSHAVLIHHRDISWDL---- 117
DB 56 VLLWVEPFGRGYKPPSPDCLRNISGCLLTDRAAYGEAQAVLFHHRDLVKELHWP 115
QY 118 -----TNLQQA-----RPPFKIWMNLESPTHTPKQSGI-EH 150
DB 116 PPWVARETDKALPVFNHKGAVTLFGKALVGRPPGQRWVWNNFSPSHSPLGLRGLAKD 175
QY 151 LFNLTLYTRDSDIQVPYGLFVSTNPFVFEVPS-----KEKLVCVVSNWNP 202
DB 176 LFNLTLYTRDSDIQVPYGLFVSTNPFVFEVPS-----KEKLVCVVSNWNP 233
QY 203 VKYKYNELSKSIEHTYGOAF-GEYVNDKNLPTISACKFYLSFENSIEHKDYITEKLY-NA 260
DB 234 VRYHQLSRVSVVDVFGAGPGRPVPAIGLLHTVARYKFLAFENSQHVVDYITEKLYNA 293

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QY 261 FLAGSPVVLGSPSRENYENIPADSFTHVEDYNSPSSEKYLKREVDKNNKLYLSYENWRK 320
DB 294 FLAGAVPVVLGPDPRANERVPFGAFTHVDFFNAASLAAYLLFLDRNVAVIRYRFRWR 353
QY 321 DFTVNLPRFWESHACLDHVK 342
DB 354 SPAVHITSFWEQWCRTCQAVQ 375

RESULT 13
O35886 PRELIMINARY; PRT; 362 AA.
AC O35886;
DT 01-JAN-1998 (T-EMBLrel. 05, Created)
DT 01-JAN-1998 (T-EMBLrel. 05, Last sequence update)
DE 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE ALPHA(1.3)FUCOSYLTRANSFERASE.
GN ALPHA(1.3)FUT.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99214609; PubMed=10187834;
RA Zhang A., Potvin B., Zaiman A., Chen W., Kumar R., Phillips L.,
RA Stanley P.;
RT "The gain-of-function chinese hamster ovary mutant LEC1B expresses
RT one of two chinese hamster FUT6 genes due to the loss of a negative
RT regulatory factor.";
RL J. Biol. Chem. 274:10439-10450(1999).
DR EMBL; U78737; AAB64355.1; -.
DR InterPro; IPR001503; Glyco_transf_10.
DR Pfam; PF00852; Glyco_transf_10; 1.
KW Transferase; Glycosyltransferase.
SQ SEQUENCE 362 AA; 41810 MW; A67940D57D47004C CRC64;

Query Match 34.8%; Score 685; DB 11; Length 362;
Best Local Similarity 41.1%; Pred. No. 2.7e-45;
Matches 147; Conservative 67; Mismatches 124; Indels 20; Gaps 10;

QY 10 RPLVICILGCMACLLIYIKPTNSWIFSPMESASSVLKMKNFSTKTDYF-NEITVLY 68
DB 14 RPLGLILLQLLFCFSSIRVSHDQGGPPADSST-----GPASTPTTPVPRPFIILL 68
QY 69 WYVFPQTGTLTSCQAMF-NIOGCHLTDRSLYNKSHAVLIHHRDISWDLTN-LPQARP. 126
DB 69 WTAFHRPLTLYPCSKMLPCTADCQMTVNRSLYPOQADAVIFHREISPNRSLLPQRP 128
QY 127 PFQKWIWMNLESTHTPQKSGIEHLNLTLYRRSDIQVYGLTVSTNPFV---FEVP 183
DB 129 PGQRWVWFSLESFSSHCRLSALDGYNLMTSYRSDSDFITPYGWLFPWAEPPVQTQVNS 188
QY 184 SKEKLVCVVYNNPNNHARVYKYNELSKSTEIHTYQAGFGEYVNDKNIPTISACKFYL 243
DB 189 AKTDLVANAVSNWNNPKSARVLYYQKLSHLVDVYGRGHP-LSRGDMGLTARYFYLA 247
QY 244 FENSIHKDYITEKLY-NAFLAGSPVVLGSPSRENYENIPADSFTHVEDYNSPSSEKYL 302
DB 248 FENSLHPDYITEKLWKNALAWAVPVVLGSPSRKNYERFLPPDAFIHVDDEFSPADLAQYL 307
QY 303 KEVDKNNKLYLSTFNWRKDTVNLPRFWESHA---CLACDHVRKHQBYKVGNEKWF 357
DB 308 QKLDKDSQSYQRYFRWRETLR---PRL-SSMALAFQACQRLQDQWLDQRYQTVHVSASF 361

RESULT 14
Q920W0 PRELIMINARY; PRT; 390 AA.
AC Q920W0;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
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DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE ALPHA 1.3-FUCOSYLTRANSFERASE (FRAGMENT).
GN FUT4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=B6M/2MSF;
RA Liu Y., Kitano T., Koide T., Shiroishi T., Moriaki K., Saitou N.;
RT "Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes of
RT Five Mus musculus subspecies.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB039125; BAB68649.1; -.
KW Transferase; Glycosyltransferase.
FT NON_TER 1
FT NON_TER 390
SQ SEQUENCE 390 AA; 44435 MW; EE7FAE238A5F9530 CRC64;

Query Match 34.8%; Score 685; DB 11; Length 390;
Best Local Similarity 42.1%; Pred. No. 2.9e-45;
Matches 142; Conservative 49; Mismatches 94; Indels 52; Gaps 8;

QY 66 ILVWVMPF---GOTFDLTSCQAMFNIQGCCHLTDRSLYNKSHAVLIHHRDISWDLTNLP 121
DB 56 VLLWVEPFRGRGYPKSPDPDCSLRFNISGCRLLTDRAAYGEAQAVLFPHHRLDLVKELDWP 115
QY 122 QQ-----ARPPFQKWIWMNLESTHTPQKSG 147
DB 116 PWCARERTDKALVLRVDFDDQEGAVTLTGKALETVGSRPQQRWVWNNFSPSTHTPLRG 175
QY 148 I-EHLFNLTLYRRSDIQVYGLTVSTNPFVFEVPS-----KEKLVCVVYNNPNN 198
DB 176 LAKDLFNWLTSLYRSDSDVFPYGLYLSRSDP--TEQPSGLGPQLARKRGLVAVVYVSNWE 233
QY 199 EHARVYKYNELSKSTEIHTYQCAF-GEYVNDKNIPTISACKFYLSTFENSHTKDYITEKL 257
DB 234 HQARVYHQLSRHVSVDVFGTPGRPVPAIGLLHVVARYKFYAFENSRHVDYITEKL 293
QY 258 Y-NAFLAGSPVVLGSPSRENYENIPADSFTHVEDYNSPSSEKYLKREVDKNNKLYSYF 316
DB 294 WRNFALAGVPVVLGPDPRANERVPFGAFTHVDFFNAASLAAYLLFLDRNVSRYRYF 353
QY 317 NWKRDFTVNLPRFWESHACLDHVKRH-QEYKSVGN 352
DB 354 RWRSEFAVHITSFWEQWCRTCQAVQTSQDQPKSIHN 390

RESULT 15
Q920W1 PRELIMINARY; PRT; 390 AA.
AC Q920W1;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE ALPHA 1.3-FUCOSYLTRANSFERASE (FRAGMENT).
GN FUT4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/10SNJ;
RA Liu Y., Kitano T., Koide T., Shiroishi T., Moriaki K., Saitou N.;
RT "Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes of
RT Five Mus musculus subspecies.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB039124; BAB68648.1; -.
KW Transferase; Glycosyltransferase.
FT NON_TER 1
FT NON_TER 390
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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	691.5	35.1	405	1	US-07-914-281-8	Sequence 8, Appli
2	691.5	35.1	405	1	US-08-393-246-8	Sequence 8, Appli
3	691.5	35.1	405	1	US-08-525-058A-8	Sequence 8, Appli
4	691.5	35.1	405	2	US-08-696-731-8	Sequence 8, Appli
5	691.5	35.1	405	4	US-09-042-531-8	Sequence 8, Appli
6	677.5	34.4	405	2	US-08-483-151-4	Sequence 4, Appli
7	670	34.0	299	5	PCR-US91-00899-6	Sequence 6, Appli
8	670	34.0	361	1	US-07-914-281-2	Sequence 2, Appli
9	670	34.0	361	1	US-08-393-246-2	Sequence 2, Appli
10	670	34.0	361	1	US-08-273-411-3	Sequence 3, Appli
11	670	34.0	361	1	US-08-525-058A-2	Sequence 2, Appli
12	670	34.0	361	2	US-08-696-731-2	Sequence 2, Appli
13	670	34.0	361	4	US-09-042-531-2	Sequence 2, Appli
14	670	34.0	361	5	PCR-US91-00899-7	Sequence 7, Appli
15	670	34.0	374	1	US-07-914-281-11	Sequence 11, Appli
16	670	34.0	374	1	US-08-393-246-11	Sequence 11, Appli
17	670	34.0	374	1	US-08-525-058A-11	Sequence 11, Appli
18	670	34.0	374	2	US-08-696-731-11	Sequence 11, Appli
19	670	34.0	374	4	US-09-042-531-11	Sequence 11, Appli
20	665.5	33.8	359	1	US-07-914-281-14	Sequence 14, Appli
21	665.5	33.8	359	1	US-08-393-246-14	Sequence 14, Appli
22	665.5	33.8	359	1	US-08-525-058A-14	Sequence 14, Appli
23	665.5	33.8	359	2	US-08-696-731-14	Sequence 14, Appli
24	665.5	33.8	359	4	US-09-042-531-14	Sequence 14, Appli
25	651.5	33.1	357	5	PCR-US91-00899-14	Sequence 14, Appli
26	582	29.5	342	2	US-08-483-151-2	Sequence 2, Appli
27	103.5	5.3	1088	2	US-08-742-026-2	Sequence 2, Appli

QY 15 VCIILGCFMAC--LLIYI---KPTNS

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Query Match      35.1%; Score 691.5; DB 1; Length 405;
Best Local Similarity 38.8%; Pred. No. 2.1e-58;
Matches 154; Conservative 58; Mismatches 110; Indels 75; Gaps 14;

y      15 VCIILGCFMAC--LLIYI---KPNNSWFSPMESASSVLKMKNFSTKTDFYFNETTILV 68
      |||:  :  |||:  :  |||:  :  |||:  :  |||:  :  |||:  :  |||:  :

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Db 28 VCVLAAGLCTALITYACWQQLPPLPWA-SPTPS-----RPGVLL 68
Qy 69 WVPFGOTFDL-----TSCQAMFNIOGCHLTDRSLYNKSHAVLIHHRDI-----SW----- 115
Db 69 WVEPFGGRDSAPRPPPCPLRFNISGCRLLTDRASYGEAQAVLFHHRDLVKGPDPWPPW 128
Qy 116 -----DLTNLPQO-----ARPPFKWIWMNLESPTHTP-QKSGIEHL 151
Db 129 GIOAHTAEVDLRVLYEAAAAAALATSSRPPGQRWVMNFESPSPGLRSLASNL 188
Qy 152 FNLTLYRDSIOVPYGFVLTSTNPFVFEVPS-----KEKLYCWMVSNWNPHEARV 203
Db 189 FNWTLRYADSDVFPYGYLYPRSHP--GDPPSGLAPPLSRKQGLVAVVWSHWDERQARV 246
Qy 204 KYNELSKSIEIHTYQOAF-GEYVNDKNLIPTISTCKFYLSFENS IHKDYITEKLY-NAF 261
Db 247 RYHOLSQHVTVDFGRGQGPVPEIGLLHTVARYKYLAFAENSQHLDTITEKLRNAL 306
Qy 262 LAGSVVVLGPRSENENYIPADSFIVHEDFNPSSELAKEYLKEVDKNNKLYLSYFNWRKD 321
Db 307 LAGAVVVLGPDPRANYERFVPRGAFIHVDFFPSASSLASYLFLDRNPAYVRYRHFHRRS 366
Qy 322 FTVNLPWFESHACLADHKVRHQEY-KSVGNLEKWF 357
Db 367 YAVHITSEWDEPWCRCVQAVQVQAGDRPKSIRNLASWF 403

RESULT 2
US-08-393-246-8
; Sequence 8, Application US/08393246
; Patent No. 5595900
; GENERAL INFORMATION:
; APPLICANT: LOWE, JOHN B.
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
; OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS.
; TITLE OF INVENTION: GLYCOPOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
; OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTURES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: P.C. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; STREET: 1755 JEFFERSON DAVIS HIGHWAY, MAIER & NEUSTADT,
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/393,246
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/220,433
; FILING DATE: 30-MAR-1994
; APPLICATION NUMBER: US 07/914,281
; FILING DATE: 20-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavalleye, Jean-Paul M. P.
; REGISTRATION NUMBER: 31,451
; REFERENCE/DOCKET NUMBER: 2363-060-55
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; INFORMATION FOR SEQ ID NO: 8:
; LENGTH: 405 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
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; MOLECULE TYPE: protein
US-08-393-246-8
Query Match 35.1%; Score 691.5; DB 1; Length 405;
Best Local Similarity 38.8%; Pred. No. 2.1e-58;
Matches 154; Conservative 58; Mismatches 110; Indels 75; Gaps 14;

Qy 15 VCIILGCFMAC--LLIYI---KPTNSWVFSPMESASSVLKMKNEFFSTKYDYFNETTILV 68
Db 28 VCVLAAGLCTALITYACWQQLPPLPWA-SPTPS-----RPGVLL 68
Qy 69 WVPFGOTFDL-----TSCQAMFNIOGCHLTDRSLYNKSHAVLIHHRDI-----SW----- 115
Db 69 WVEPFGGRDSAPRPPPCPLRFNISGCRLLTDRASYGEAQAVLFHHRDLVKGPDPWPPW 128
Qy 116 -----DLTNLPQO-----ARPPFKWIWMNLESPTHTP-QKSGIEHL 151
Db 129 GIOAHTAEVDLRVLYEAAAAAALATSSRPPGQRWVMNFESPSPGLRSLASNL 188
Qy 152 FNLTLYRDSIOVPYGFVLTSTNPFVFEVPS-----KEKLYCWMVSNWNPHEARV 203
Db 189 FNWTLRYADSDVFPYGYLYPRSHP--GDPPSGLAPPLSRKQGLVAVVWSHWDERQARV 246
Qy 204 KYNELSKSIEIHTYQOAF-GEYVNDKNLIPTISTCKFYLSFENS IHKDYITEKLY-NAF 261
Db 247 RYHOLSQHVTVDFGRGQGPVPEIGLLHTVARYKYLAFAENSQHLDTITEKLRNAL 306
Qy 262 LAGSVVVLGPRSENENYIPADSFIVHEDFNPSSELAKEYLKEVDKNNKLYLSYFNWRKD 321
Db 307 LAGAVVVLGPDPRANYERFVPRGAFIHVDFFPSASSLASYLFLDRNPAYVRYRHFHRRS 366
Qy 322 FTVNLPWFESHACLADHKVRHQEY-KSVGNLEKWF 357
Db 367 YAVHITSEWDEPWCRCVQAVQVQAGDRPKSIRNLASWF 403

RESULT 3
US-08-525-058A-8
; Sequence 8, Application US/08525058A
; Patent No. 5770420
; GENERAL INFORMATION:
; APPLICANT: LOWE, JOHN B.
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
; OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
; TITLE OF INVENTION: GLYCOPOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
; OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTURES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.
; STREET: 1755 JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,058A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavalleye, Jean-Paul M. P.
; REGISTRATION NUMBER: 31,451
; REFERENCE/DOCKET NUMBER: 2363-060-55
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
```

; FILING DATE: 20-JUL-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lavalleye, Jean-Paul M. P.
 ; REGISTRATION NUMBER: 31,451
 ; REFERENCE/DOCKET NUMBER: 2363-060-55
 ; TELECOMMUNICATION INFORMATION:
 ;

TELEPHONE: (703) 521-4500
TELEFAX: (703) 486-2347
TELEX: 248855 OPAT UR

```

; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 405 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-696-731-8

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Query Match 35.1%; Score 691.5; DB 2; Length 405;
Best Local Similarity 38.8%; Pred. No. 2.1e-58;
Matches 154; Conservative 58; Mismatches 110; Indels 75; Gaps 14;

QY	15	VCILGCFMAC--LLIYI----	RPTNSWFSFPMESASSVLKMKNFSTKTDYFNETTILV	68
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DB	28	VCVLAAGLTCTALITYACWGQLPPLPWA-SPTPS-----	RPVGVLV	68

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QY      69  WWMPFGOTFDL-----TSCQAMFNIGQCHLLTDRSLYKNKSHAVLIHHRDI-----SW----- 115
      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
Db      69  WNEPFGGRSAPRPPDPCLPURNISGCRLLITDRASYGEQAVLFHHRDLVKGPDPWPPW 128

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116 QY -----DLTNLPQ-----ARPPFKWIMNLESPHTP-QKSGIEHL 151
      || | : || | : || | : || | : || | : || | : || | : || | :
129 Db QIQAHTAEVDLVLVDYEAAAAAALATSPRPPGQRWVMNFPESPSPGLRSLASNL 188

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152  FNLTLTYYRRSDIQVYGFGLTVSTNPVFVPS-----KEKLVGVVYVNNNPEHARV  203
    || ||||| |||: |||||: ||: ||: || |||||: |||
189  FNWTLVSRADSDVFPVGYLYPRSHP--GDPPGSLAPPLSRKQGLVAVVYVSHWDERQARV  246

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QY 204 KYNELSKSEIHTYGAAF-GEYVNDKNLPTISTCKFYLSFENSIIHKDIYTEKLY-NAF 261
:::||||: : :: | : : : |||:|||| | |||||: ||
Db 247 RYHQQLSQHVTVDVFGRGGPGQPPEGLGTHTVARYKFYLAFENSOHLDIYTEKLWRNAL 306

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262 LAGSVPTVLGSPRENENYIPADSFIVEDFNPSSELAKYLKEVDKNNKLYLSYFNWRKD 321
   |||:||||||| ||| ::| :|||:| | | | | | | | | | | | | | | | | | | |
307 LAGAVPTVLGPDANRNERFVPRGAFIHVDVDFPSASSLASVLLFLDNRPNVYRYFHWRRS 366

```

QY 322 FTVNLPWFESHACLADHVKRHQEY - KSVGNLEKWF 357
: : : | : : : : : : :
Db 367 YAVHIISFWDPEWCRVCOAQRAGDRPKSTRNLASWF 403

RESULT 5
US-09-042-531-8

; Sequence 8, Application US/09042531
 ; Patent No. 6268193
 ; GENERAL INFORMATION:
 ; APPLICANT: LOWE, JOHN B.

;	TITLE OF INVENTION:	METHODS AND PRODUCTS FOR THE SYNTHESIS
;	TITLE OF INVENTION:	OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
;	TITLE OF INVENTION:	GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLAT
;	TITLE OF INVENTION:	OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRU

NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.

STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.

```

; *****
;
;      ZIP:  22202
;
;      COMPUTER READABLE FORM:
;
;      MEDIUM TYPE: Floppy disk
;
;      COMPUTER: IBM PC compatible

```

```

; COME FROM: IBM PC COMPACT
; OPERATING SYSTEM: PC-DOS/MS-DOS

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Db	240	RYEYLAFAENSLHPDYITEKLWRNALAEAWPVVLGPRSNTERFLPDDAFTHVDDFQSP	299
QY	296	SELAKEYVDKNNKLYLSYFNWRKDEFTVNLPR--FWESHACIACDHVKRHOEYKSVGNL	353
Db	300	KDLAYQLDKDHARYLSYFRWRETLR--PRSFSWALDFCKACWKLOQESRYQTVRSI	356
QY	354	EKWF	357
Db	357	AAWF	360

RESULT 11
 US-08-525-058A-2
 ; Sequence 2, Application US/08525058A
 ; Patent No. 5770420
 ; GENERAL INFORMATION:
 ; APPLICANT: LOWE, JOHN B.
 ; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
 ; TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
 ; TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
 ; TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTURES
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: OBLOH, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
 ; STREET: 1755 Jefferson Davis Highway, Fourth Floor
 ; CITY: Arlington
 ; STATE: Virginia
 ; COUNTRY: U.S.A.
 ; ZIP: 22202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/525,058A
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lavalleye, Jean-Paul M. P.
 ; REGISTRATION NUMBER: 31,451
 ; REFERENCE/DOCKET NUMBER: 2363-060-55
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703)521-4500
 ; TELEFAX: (703)486-2347
 ; TELEX: 248855 OPAT UR
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 361 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-525-058A-2

```

QY    296 SELAKYKEVDKNNKLHSLTFNRKRDTVMNLP--FWESHACIACDHVKRHKQYSVGNL   353
      :|||::|::|:: |::|::|:: || | | | :: |::|::
Db    300 KDALRYQLDKDGHARYLSYFRWRETLR---PRFSWALDFCKACKWKLOQRSYTIVRSI   356
      QY    354 EKWF 357
      Db    357 AAWF 360

RESULT 12
US-08-696-731-2
; Sequence 2, Application US/08696731
; Patent No. 5955347
; GENERAL INFORMATION:
; APPLICANT: LOWE, JOHN B.
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
;     OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
;     TITLED OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
;     OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCU
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OHLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/696,731
; FILING DATE: 14-AUG-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/393,246
; FILING DATE:
; APPLICATION NUMBER: US 08/220,433
; FILING DATE: 30-MAR-1994
; APPLICATION NUMBER: US 07/914,281
; FILING DATE: 20-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavallee, Jean-Paul M. P.
; REGISTRATION NUMBER: 31,451
; REFERENCE/DOCKET NUMBER: 2363-060-55
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-696-731-2
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Query Match	34.0%;	Score 670;	DB 2;	Length 361;
Best Local Similarity	43.4%;	Pred. No. 2.1e-56;		
Matches 132;	Conservative 54;	Mismatches 98;	Indels 20;	Gaps

QY	66	ILVWVPFGTDLTSCQAMF-NIQCHLTTRSLYKNSHAVLIHHRDTSWDL-----TN	119
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		: :	:
		: :	:
Db	65	ILLTWTFPHIPVALSRCSEMPVGTADCHITADKKVYQADTVIVHH---WDIMSPKSR	120
		:	:
		: :	:
		: :	:
QY	120	LPQQAAPPQKWLMMNLESPHTPTQKSGTEHLFNLTLTTRRSDTQVPGFTLV-STWPF	178
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		: :	:
Db	121	LPSPRPQGORWTFNLEPPNQCULEADVFNLTMSYRSDSTFTYQVLEPWSGQPA	180
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QY 179 --VEFVPSKEKLVGVVSNMNPHEARVYKYNELSKSIEIHTYGOAFGEYVNDKNLIPTIS 236
Db 181 HPLNLSAKTELVAWAVSNMNPDSARVYQSLQAHKLVGVGRSH-KPLPKGTMETLS 239
QY 237 TCKFYLSFENSIIHKDYITEKLY-NAFLAGSVPVVGLPSRENYENYIPADSFIVHEDFNSP 295
Db 240 RYKFLAFENSLHPDYITEKLNRNALEAWAVPVVGLPSRSNYERFLPPDAFIHVDDFQSP 299
QY 296 SELAKYLKEVDKNNKLYSYFNWRKDFVNLPR--FWESHACIACDHRVHRHQBKYSVGNL 353
Db 300 KDLARYLQELDKDHARYLSYFRWRETLR---PRSFWSALDFCKACWKLOQESRYQTVRSI 356
QY 354 EKWF 357
Db 357 AAWF 360

RESULT 13
US-09-042-531-2
; Sequence 2, Application US/09042531
; Patent No. 6268193
; GENERAL INFORMATION:
; APPLICANT: LOWE, JOHN B.
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
; OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
; TITLE OF INVENTION: GLYCOPOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
; OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,531
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/393,246
; FILING DATE:
; APPLICATION NUMBER: US 08/220,433
; FILING DATE: 30-MAR-1994
; APPLICATION NUMBER: US 07/914,281
; FILING DATE: 20-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavalleye, Jean-Paul M. P.
; REGISTRATION NUMBER: 31,451
; REFERENCE/DOCKET NUMBER: 2363-060-55
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-09-042-531-2

Query Match 34.0%; Score 670; DB 4; Length 361;
Best Local Similarity 43.4%; Pred. No. 2.1e-56;
Matches 132; Conservative 54; Mismatches 98; Indels 20; Gaps 9;

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QY 120 LPQARPPFQKWIWNLESPTHTPKSGIEHLFNLTLYRRSDIQVPYGLTV-STNPF 178
Db 121 LPPSRPGQGWIFNLEPPPCQHLALDRYFNLTMSYRSDSDIFTTYPGWLEPWSQGA 180
QY 179 --VEFVPSKEKLVGVVSNMNPHEARVYKYNELSKSIEIHTYGOAFGEYVNDKNLIPTIS 236
Db 181 HPLNLSAKTELVAWAVSNMNPDSARVYQSLQAHKLVGVGRSH-KPLPKGTMETLS 239
QY 237 TCKFYLSFENSIIHKDYITEKLY-NAFLAGSVPVVGLPSRENYENYIPADSFIVHEDFNSP 295
Db 240 RYKFLAFENSLHPDYITEKLNRNALEAWAVPVVGLPSRSNYERFLPPDAFIHVDDFQSP 299
QY 296 SELAKYLKEVDKNNKLYSYFNWRKDFVNLPR--FWESHACIACDHRVHRHQBKYSVGNL 353
Db 300 KDLARYLQELDKDHARYLSYFRWRETLR---PRSFWSALDFCKACWKLOQESRYQTVRSI 356
QY 354 EKWF 357
Db 357 AAWF 360

RESULT 14
PCT-US91-00899-7
; Sequence 7, Application PC/TUS9100899
; GENERAL INFORMATION:
; APPLICANT: LOWE, John B.
; TITLE OF INVENTION: Method and Products For the Synthesis of
; OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS, GLYCOPOLIPIDS,
; TITLE OF INVENTION: or as Free Molecules, and For the Isolation of Cloned
; TITLE OF INVENTION: Genetic Sequences That Determine These Structur
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/00899
; FILING DATE: 19910214
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavalleye Ph.D., Jean-Paul
; REGISTRATION NUMBER: 31,451
; REFERENCE/DOCKET NUMBER: 2363-021-55 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-5940
; TELEFAX: (703)486-2347
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: Blood
; CELL LINE: A431
PCT-US91-00899-7

Query Match 34.0%; Score 670; DB 5; Length 361;
Best Local Similarity 43.4%; Pred. No. 2.1e-56;

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 8, 2002, 15:05:27 ; Search time 42.5 Seconds
(without alignments)
938.247 Million cell updates/sec

Title: US-09-744-748-2
Perfect score: 1970
Sequence: 1 MTSISKGILRFLIWCILG.....HVKRHQEYKSVNLEKFWFN 359

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1970	100.0	359	21	AA1980996
2	1961	99.5	359	21	AA1980995
3	689.5	35.0	405	11	AA19808119
4	689.5	35.0	405	12	AA19808119
5	689.5	35.0	405	12	AA19808119
6	689.5	35.0	405	12	AA19808119
7	689.5	35.0	405	12	AA19808119
8	689.5	35.0	405	12	AA19808119
9	689.5	35.0	405	12	AA19808119
10	689.5	35.0	405	12	AA19808119
11	676	34.3	360	18	AA19808119

12	675	34.3	360	18	AA19808119	Human chimeric fuc
13	674	34.2	361	18	AA19808119	Human chimeric fuc
14	673	34.2	361	18	AA19808119	Human chimeric fuc
15	672	34.1	361	18	AA19808119	Human chimeric fuc
16	671	34.1	360	18	AA19808119	Human chimeric fuc
17	669.5	34.0	359	18	AA19808119	Human chimeric fuc
18	669.5	34.0	360	18	AA19808119	Human chimeric fuc
19	668	34.0	496	15	AA19808119	A glycosyltransferase
20	668	33.9	361	18	AA19808119	Human chimeric fuc
21	667	33.9	361	12	AA19808119	GDP-Fuc:[beta-D-Ga
22	667	33.9	361	15	AA19808119	A glycosyltransferase
23	667	33.9	361	18	AA19808119	Human alpha 1,3/4
24	667	33.9	361	18	AA19808119	Human chimeric fuc
25	667	33.9	361	18	AA19808119	Human alpha(1,3)/1,
26	667	33.9	361	22	AA19808119	Human Lewis enzyme
27	667	33.9	374	15	AA19808119	A glycosyltransferase
28	667	33.9	374	18	AA19808119	Human alpha(1,3)-f
29	662.5	33.6	359	15	AA19808119	Alpha-(1-3)Fuc-Tv1
30	662.5	33.6	359	18	AA19808119	Human chimeric fuc
31	662.5	33.6	359	18	AA19808119	Human alpha(1,3)-f
32	661.5	33.5	359	18	AA19808119	Human chimeric fuc
33	660.5	33.5	360	18	AA19808119	Human chimeric fuc
34	660	33.5	361	18	AA19808119	Human chimeric fuc
35	658.5	33.4	360	18	AA19808119	Human chimeric fuc
36	657.5	33.4	359	18	AA19808119	Human chimeric fuc
37	656.5	33.3	359	18	AA19808119	Human chimeric fuc
38	655.5	33.3	359	18	AA19808119	Human chimeric fuc
39	654.5	33.2	360	18	AA19808119	Human chimeric fuc
40	653.5	33.2	360	18	AA19808119	Human chimeric fuc
41	622	31.6	342	15	AA19808119	Human alpha-1,3-fu
42	619	31.4	342	20	AA19808119	Human alpha1,3-fuc
43	605.5	30.7	350	18	AA19808119	Human chimeric fuc
44	580	29.4	342	18	AA19808119	Murine myeloid-lin
45	579	29.4	342	18	AA19808119	Mouse alpha-fucosy

ALIGNMENTS

RESULT 1
AA1980996
ID AA1980996 standard; Protein; 359 AA.
XX
AC AA1980996;
XX
DT 05-JUN-2000 (first entry)
XX
DE Human alpha-1,3-fucosyltransferase.
XX
KW Alpha-1,3-fucosyltransferase; fucose; glycosylation; Lewis epitope;
KW brain; kidney; recombinant expression; transgenic animal; knockout
KW animal; FUC-TIV; drug screening; inhibitor; potentiator; diagnosis;
KW treatment; cancer; human.
XX
OS Homo sapiens.
XX
PN WO200006708-A1.
XX
PD 10-FEB-2000.
XX
PF 29-JUL-1999; 99WO-JP04092.
XX
PR 29-JUL-1998; 98JP-0213823.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Narimatsu H, Kudo T, Sasaki K;
XX
DR WPI; 2000-183120/16.
XX
DR N-PSDB; AA292646, AA292647.
XX
PT Alpha 1,3-fucosyltransferase generating Lewis x but not sialyl-Lewis x
PT epitope and an antibody recognizing it useful for diagnosis of brain

QY 241 YLSFENSIKDYITEKLYNAFLAGSVVVLGSPRENYENYIPADSFHVEDYNSPSELAK 300
DB 241 YLSFENSIKDYITEKLYNAFLAGSVVVLGSPRENYENYIPADSFHVEDYNSPSELAK 300
QY 301 YLKEVDKNNKLYLSYFNWRKDFVNLPRWESHACIACDHRVHQRQYKSVGNLEKWFN 359
DB 301 YLKEVDKNNKLYLSYFNWRKDFVNLPRWESHACIACDHRVHQRQYKSVGNLEKWFN 359

RESULT 3
AAR08119
ID AAR08119 standard; protein; 405 AA.
AC AAR08119;
XX
XX 27-FEB-1991 (first entry)
XX CDX, a MILA involved in ELAM1-mediated adhesion, from pCDM8 clone 7.2.
XX Endothelial cell-leucocyte adhesion molecule 1; ELAM1; CDX;
KW molecule involved in leucocyte adhesion; MILA; inflammation.
XX
XX Homo sapiens.
XX
XX W09013300-A.
XX
XX 15-NOV-1990.
XX
XX 27-APR-1990; 90WO-US02357.
XX
XX 18-DEC-1989; 89US-0452675.
XX 28-APR-1989; 89US-0345151.
XX 01-JUN-1989; 89US-0359516.
XX
XX (BIOG-) BIOGEN INC.
XX
XX Hession C, Lobb RR, Goelz SE, Born L, Benjamin CD;
PI Rosa MD;
XX
XX WPI; 1990-361248/48.
XX N-PSDB; AAQ06691.
XX
XX Endothelial cell adhesion mols. - MILAS and DNA encoding them and
PT inhibition-detection of binding of leukocytes to endothelial
PT cells
XX
XX Disclosure; Fig 9 (A-C); 136pp; English.
XX
XX CDX is a MILA, involved in ELAM1-mediated adhesion and is probably
CC the (or an) ELAM1 ligand. CDX is expressed in melanomas.
CC See also AAQ06686-91.
XX
XX Sequence 405 AA;

Query Match 35.0%; Score 689.5; DB 11; Length 405;
Best Local Similarity 38.5%; Pred. No. 4.5e-54;
Matches 153; Conservative 60; Mismatches 109; Indels 75; Gaps 14;

QY 15 VCIIILGCFMAC--LLIYI----KPTNSWIFSPMESASSVLKMKNFSTKTDYFNWTILV 68
DB 28 VCVLAAGLTCTALITYACWGQLPPLPWA-SPTPS-----RPVGVLL 68

QY 69 WVPFGQTDL----TSCQAMFIQGCGLTTRSLYNKSHAVLIHHRDI-----SW---- 115
DB 69 WVEPFGGDSAPRPPDCLRLRENFISCRLLTDRASYGEAQLVHHRDLVKGPPDPWPPW 128

QY 116 -----DLNLPQQ-----ARPPQKWITWMNLESPHTTP-OKSGIEHL 151
DB 129 GIOHTAEYDLRLVLDYEEAAAAAALATSSPRPPGQRYWMNFSPSHSPGLRSLASNL 188

QY 152 FNLTFLYRRSDIQVPYGFVLTNTNPFVFPVS-----KEKLYCWVYNNPNPHARY 203
DB 152 FNLTFLYRRSDIQVPYGFVLTNTNPFVFPVS-----KEKLYCWVYNNPNPHARY 203

DB 189 FNTLSYRADSDVFPYGYLYPRSHP--GDPPSLAPPLSRKQGLVAVVSHWDERQARV 246
QY 204 KYNEISKSIEHTYQAF-GEYVNDKNLIPTISACKFYLSFENSIHKDYITEKLY-NAF 261
DB 247 RYXHQLSQHVTVDFGRGGPGQVPEIGLHTVARYKFKYLAFAENSQHLDTITEKLWRNAL 306
QY 262 LAGSVVVLGSPRENYENYIPADSFHVEDYNSPSELAKYLVKEDKNNKLYLSYFNWRKD 321
DB 307 LAGAVPVVLGPDPRANYERFVPRGAFIHVDDFPSASSLASLYLLFLDRPNPAYERFYHWRKS 366
QY 322 FTVNLPFRWFESHACIACDHRVHQRQY-KSVGNLEKWF 357
DB 367 YAVHITSFWDPCRVQAVORAGDRPKSIRNLASWF 403

RESULT 4
AAR13752
ID AAR13752 standard; Protein; 405 AA.
XX
XX AAR13752;
XX
XX 07-NOV-1991 (first entry)
XX
XX GDP-Fuc:beta-D-Gal(1,4)-D-GlcNAc alpha(1,3)-fucosyltransferase.
XX
XX Glycosyltransferase.
XX
XX Homo sapiens.
XX
XX W09112340-A.
XX
XX 22-AUG-1991.
XX
XX 14-FEB-1991; 91WO-US00899.
XX
XX 12-DEC-1990; 90US-0627621.
XX 14-FEB-1990; 90US-0479858.
XX 14-FEB-1990; 90US-0480133.
XX
XX (UNMI) UNIV OF MICHIGAN.
XX
XX Lowe JB;
XX
XX WPI; 1991-267151/36.
XX N-PSDB; AAQ13333.
XX
XX Isolation of gene conveying post-translational characteristic -
PT e.g. the presence of soluble or membrane bound oligo or
PT polysaccharide or glycosyltransferase.
XX
XX Disclosure; Fig 4; 155pp; English.
XX
XX The amino acid sequence codes for a protein capable of functioning
CC as a GDP- Fuc:(beta-D-Gal(1,4)-D-GlcNAc alpha(1,3)-fucosyl-
CC transferase. The functional protein is represented by amino acids
CC 50 to 405. The enzyme when expressed by the cloned DNA sequence
CC functions within mammalian cells to generate new expression of
CC specific cell surface glyco-conjugate structures of those cells.
CC It can be used to construct animal cell lines to act as host cells
CC for the prodn. of diagnostic or therapeutic materials whose
CC usefulness or efficacy depends upon the specific post-translational
CC modification determined by the cloned DNA sequence and its encoded
CC enzyme. See also AAR13749-R13751.
XX
XX Sequence 405 AA;

Query Match 35.0%; Score 689.5; DB 12; Length 405;
Best Local Similarity 38.5%; Pred. No. 4.5e-54;
Matches 153; Conservative 60; Mismatches 109; Indels 75; Gaps 14;

QY 15 VCIIILGCFMAC--LLIYI----KPTNSWIFSPMESASSVLKMKNFSTKTDYFNWTILV 68
DB 28 VCVLAAGLTCTALITYACWGQLPPLPWA-SPTPS-----RPVGVLL 68

QY 69 WWPFGQTFDL-----TSCQAMENIOGCHLTDRSLYNKSHAVLIHHRDI-----SW----- 115
 DB 69 WWPFGGRDSAPRPDPCLRFNISGCRLLTDRASYGEAQVLFHHRDLVKGPPDPWPPW 128
 QY 116 -----DLTNLPQ-----ARPPQKIWMNLESPTHTP-QKSGIEHL 151
 DB 129 GIOHTAEVDLRLVDEEAAAALATSSRPPGQKRWVWVFESHSPLSLASNL 188
 QY 152 FNLTYRRDSIOQVYGFGLTVSTNPFVFEVPS-----KEKLVCVVSNWNPHEHARV 203
 DB 189 FNMWLSYRADSDVFPYGYLYPRSHP--GDPPSGLAPPLSRKQGLVAVVWSHMDERQARV 246
 QY 204 KYNELSKSIEIHTYGOAF-GEYVNDKNLIPTISACKFYLSFENSIIHKDYITEKLY-NAF 261
 DB 247 RYHOLSHQVTVDFVGRGPGQVPEIGLLHTVARYKFLAFENSQHLDTYITEKLWRNAL 306
 QY 262 LAGSVPVVLGPRSRENYENIYPADSFIHVEDYNSPSELAKYLKEVDKNNKLYLSYFNWRKD 321
 DB 307 LAGAVPVVLGPDRAHYERFVPRGAFIHVDDFPSASSLASYLFLDRNPVARYRYFHWRRS 366
 QY 322 FTVNLPWFESHACIADHVKKRHOEY-KSVGNLEKWF 357
 DB 367 YAVHITSEWDEPWCRCVQAVQVQAGDRPKSIRNLASWF 403

RESULT 5

AAR14404
 ID AAR14404 standard; Protein; 405 AA.

AC AAR14404;

DT 13-FEB-1992 (first entry)

DE Protein 7.2 (1.3-fucosyl transferase).

KW CDX; cell adhesion; ELAM1.

OS Homo sapiens.

PN WO9116900-A.

PD 14-NOV-1991.

PF 26-OCT-1990; 90WO-US06198.

PR 27-APR-1990; 90WO-US02357.

PR 26-OCT-1990; 90WO-US06198.

PA (BIOJ) BIOGEN INC.

PI Goelz SE, Hession CA;

DR WPI; 1991-353507/48.

DR N-PSDB; AAQ14382.

PT DNA sequences encoding 1,3-fucosyl transferase - used to develop

PT antiinflammatory therapy by inhibition of linking activity.

PS Claim 23; Fig 1; 38pp; English.

CC The sequence was deduced from CDX pCDM8 clone 7.2 and from a
 CC portion of the 7.2 insert subcloned into the sequencing vector
 CC pNN1 to prepare pSQ219. The protein, a 1,3-fucosyl transferase is
 CC a surface glycoprotein which is recognised by anti-CDX antibodies
 CC and which binds to ELAM1. The sequence is identical to the portion
 CC of protein 1 (encoded by clone 1; AAQ14383) from residue 126-530.
 CC The two proteins may represent different transcripts from the same
 CC DNA segment. The protein may be useful in the development of anti-
 CC inflammatory or other therapies.
 CC See also AAR14405.

XX Sequence 405 AA;

Query Match 35.08; Score 689.5; DB 12; Length 405;
 Best Local Similarity 38.58; Pred. No. 4.5e-54;
 Matches 153; Conservative 60; Mismatches 109; Indels 75; Gaps 14;

QY 15 VCIILGCFMAC--LLIYI---KPTNSWIFSPMESASVLMKKNFFSTKTDYFNETILV 68
 DB 28 VCVLAAAGLCTCTALITACWGQLPLPWA-SPTPS-----RPVGVLL 68
 QY 69 WWPFGQTFDL-----TSCQAMENIOGCHLTDRSLYNKSHAVLIHHRDI-----SW----- 115
 DB 69 WWPFGGRDSAPRPDPCLRFNISGCRLLTDRASYGEAQVLFHHRDLVKGPPDPWPPW 128
 QY 116 -----DLTNLPQ-----ARPPQKIWMNLESPTHTP-QKSGIEHL 151
 DB 129 GIOHTAEVDLRLVDEEAAAALATSSRPPGQKRWVWVFESHSPLSLASNL 188
 QY 152 FNLTYRRDSIOQVYGFGLTVSTNPFVFEVPS-----KEKLVCVVSNWNPHEHARV 203
 DB 189 FNMWLSYRADSDVFPYGYLYPRSHP--GDPPSGLAPPLSRKQGLVAVVWSHMDERQARV 246
 QY 204 KYNELSKSIEIHTYGOAF-GEYVNDKNLIPTISACKFYLSFENSIIHKDYITEKLY-NAF 261
 DB 247 RYHOLSHQVTVDFVGRGPGQVPEIGLLHTVARYKFLAFENSQHLDTYITEKLWRNAL 306
 QY 262 LAGSVPVVLGPRSRENYENIYPADSFIHVEDYNSPSELAKYLKEVDKNNKLYLSYFNWRKD 321
 DB 307 LAGAVPVVLGPDRAHYERFVPRGAFIHVDDFPSASSLASYLFLDRNPVARYRYFHWRRS 366
 QY 322 FTVNLPWFESHACIADHVKKRHOEY-KSVGNLEKWF 357
 DB 367 YAVHITSEWDEPWCRCVQAVQVQAGDRPKSIRNLASWF 403

RESULT 6

AAR28840
 ID AAR28840 standard; Protein; 405 AA.

AC AAR28840;

DT 05-APR-1993 (first entry)

DE HeLa cell fucosyltransferase enzyme.

KW glycosyltransferase; galactosyltransferase; sialyltransferase;

KW fucosyltransferase; membrane bound; ss.

OS Homo sapiens.

PN GB2256197-A.

PD 02-DEC-1992.

PF 14-APR-1992; 92GB-0008211.

PR 31-MAY-1991; 91EP-0810414.

PR 04-MAR-1992; 92EP-0810167.

PR 14-APR-1992; 92GB-0008211.

PA (CIBA) CIBA GEIGY AG.

PI Berger EG, Meyhack B, Watzele G, Watzele M, Berger E;

DR WPI; 1992-401159/49.

DR N-PSDB; AAQ31434.

PT Glycosyltransferase prodn. process - includes transforming yeast

PT cells with expression cassettes contg. mammalian coding sequences

PT controlled by yeast promoters

PS Claim 16; Page 43; 65pp; English.

CC This sequence represents a fucosyltransferase enzyme from HeLa cells.

DR WPI: 1994-048874/06.
DR N-PSDB: AAQ56909.

PT DNA fragment encoding a glycosyltransferase - can be used for in
PT vitro reactions to modify cell surface oligosaccharide(s) e.g.
PT blood gp. determinants, to protect against transplant rejection

XX
XX Disclousure: Fig 4; 249pp; English.

XX The sequence is that of a human glycosyl transferase. The enzyme
CC may be non glycosylated. This prevents premature loss of enzyme
CC activity. It can also be used in in vitro reactions to modify cell
CC surface oligosaccharide mols. e.g. blood group determinants.
CC See also AAR45933-9.

XX Sequence 405 AA;

Query Match 34.8%; Score 685.5; DB 15; Length 405;

Best Local Similarity 38.5%; Pred. No. 1e-53;

Matches 153; Conservative 59; Mismatches 110; Indels 75; Gaps 14;

QY 15 VCIILGCFMAC--LLIYI-----KPTNSWIFSPMESASSVLKMKNFSTKTDYFNETTILV 68
DB 28 VCVLAAAGLTCTALITYACWGQLPLPWA-SPTPS-----RPVGVLL 68

QY 69 WWPFGQTFDL-----TSCQAMFNIOGCHLTDRSLYNKSHAVLIHHRDI-----SW----- 115
DB 69 WWPFGGRDSAPRPPDCPLRFNLSGCRLLTDRASYGQAQVLFHHRDLVKGPDPWPPW 128

QY 116 -----DLTNLPOQ-----ARPPFQKWIWNLESPTHTP-QKSGIEHL 151
DB 129 GIOAHTAEVDLRVLDYEAAAAEALATSSPRPPGQRWVWNFESPSHSPGLRSLASNL 188

QY 152 FNLTITRRSDIOVPYGLTVSTNPFVFEVPS-----KEKLVCMVWVNNNPEHARV 203
DB 189 FNWTLSTRADSDVFPYGLYPRSHP--GDPPSGLAPPLSRKQGLVAVWVSHWDDROARV 246

QY 204 KYNELSKSIETHYGOAF-GEYVNDKNLIPTISACKFYLSFENSIIHKDYITEKLY-NAF 261
DB 247 RYHQLSQHVTVDVFGGPGQVPVEIGLLHTVARYKPYLAFENSQHLDTYITEKLWRLNAL 306

QY 262 LAGSPVVLGSPRENYENIPADSFHVEDYNSPELAKYLKEVDKNNKLYLSYFNWRKD 321
DB 307 LAGAVPVVLGPDRAHYEAFVPRGAFIHVDVDFPSASSLASYLFLDLRNPAYRYFHWRRS 366

QY 322 FTVNLPFWESHACLDCHVHRHOEY-KSVGNLEKWF 357
DB 367 YAVHITSFWEDEPWCRCVQAVQAGDRPKSIRNLASWF 403

RESULT 9
AAW13641 standard; Protein; 405 AA.

XX AAW13641;

XX 19-JUN-1997 (first entry)

XX Human alpha(1,3)-fucosyltransferase (Fuc-TIV).

XX Alpha(1,3)-fucosyltransferase; Lewis enzyme; Fuc-TIV;

XX glycosylation; oligosaccharide; blood group.

XX Homo sapiens.

XX WO9709421-A1.

XX 13-MAR-1997.

XX 06-SEP-1996; 96WO-US13816.

XX 08-SEP-1995; 95US-0525058.

XX

PA (UNMI) UNIV MICHIGAN.

XX Legault DJ, Lowe JB;

XX WPI; 1997-192897/17.

XX N-PSDB; AAT61678.

XX New recombinant fucosyltransferase proteins - useful for modifying

XX cell surface oligosaccharide structures

XX Example 4; Page 284-285; 329pp; English.

XX Human GDP-Fuc-beta-D-Gal(1,4)-D-GlcNAc alpha(1,3)-fucosyltransferase

XX (Fuc-TIV) (AAW13641) can utilise type II acceptor substrates, but not

XX type I substrates, and therefore cannot form the sialyl Lewis x

XX determinant. Its amino acid sequence was deduced from an isolated

XX DNA sequence obt'd. from a human genomic DNA using Lewis enzyme cDNA

XX (see also AAT61675) as probe. the Fuc-TIV enzyme, when expressed by

XX de novo expression of specific cell surface glycoconjugate structures

XX that are recognised by antibodies against SSEA-1 or Lewis x and by an

XX antibody against the VIM-2 determinant.

XX Sequence 405 AA;

Query Match 34.8%; Score 685.5; DB 18; Length 405;

Best Local Similarity 38.5%; Pred. No. 1e-53;

Matches 153; Conservative 59; Mismatches 110; Indels 75; Gaps 14;

QY 15 VCIILGCFMAC--LLIYI-----KPTNSWIFSPMESASSVLKMKNFSTKTDYFNETTILV 68
DB 28 VCVLAAAGLTCTALITYACWGQLPLPWA-SPTPS-----RPVGVLL 68

QY 69 WWPFGQTFDL-----TSCQAMFNIOGCHLTDRSLYNKSHAVLIHHRDI-----SW----- 115
DB 69 WWPFGGRDSAPRPPDCPLRFNLSGCRLLTDRASYGQAQVLFHHRDLVKGPDPWPPW 128

QY 116 -----DLTNLPOQ-----ARPPFQKWIWNLESPTHTP-QKSGIEHL 151
DB 129 GIOAHTAEVDLRVLDYEAAAAEALATSSPRPPGQRWVWNFESPSHSPGLRSLASNL 188

QY 152 FNLTITRRSDIOVPYGLTVSTNPFVFEVPS-----KEKLVCMVWVNNNPEHARV 203
DB 189 FNWTLSTRADSDVFPYGLYPRSHP--GDPPSGLAPPLSRKQGLVAVWVSHWDDROARV 246

QY 204 KYNELSKSIETHYGOAF-GEYVNDKNLIPTISACKFYLSFENSIIHKDYITEKLY-NAF 261
DB 247 RYHQLSQHVTVDVFGGPGQVPVEIGLLHTVARYKPYLAFENSQHLDTYITEKLWRLNAL 306

QY 262 LAGSPVVLGSPRENYENIPADSFHVEDYNSPELAKYLKEVDKNNKLYLSYFNWRKD 321
DB 307 LAGAVPVVLGPDRAHYEAFVPRGAFIHVDVDFPSASSLASYLFLDLRNPAYRYFHWRRS 366

QY 322 FTVNLPFWESHACLDCHVHRHOEY-KSVGNLEKWF 357
DB 367 YAVHITSFWEDEPWCRCVQAVQAGDRPKSIRNLASWF 403

RESULT 10
AAW11821

XX AAW11821 standard; Protein; 405 AA.

XX AAW11821;

XX 06-MAY-1997 (first entry)

XX Human myeloid derived fucosyltransferase (Fuc-TIV).

XX Fucosyltransferase; Fuc-TIV; fucosylation; antibody; IgG; Igm;

XX septic shock; septicemia; therapy.

XX Homo sapiens.

XX


```
PN WO9640881-A1.
XX
PD 19-DEC-1996.
XX
XX 08-MAY-1996; 96WO-US06427.
XX
XX 07-JUN-1995; 95US-0483151.
XX
XX (GEO ) GEN HOSPITAL CORP.
XX
XX Holgersson J, Seed B;
XX
XX WPI: 1997-108639/10.
DR N-PSDB; AAT58506.
XX
XX New murine alpha-(1,3)-fucosyltransferase - for fucosylating an
PT antibody to protect mammals against e.g. septic shock or septicaemia
XX
XX Claim 17; Fig 6B; 58pp; English.
XX
XX Introduction of human myeloid cell-specific fucosyltransferase
CC Fuc-TIV (AAW11821) into a murine cell line results in the appearance
CC of a fucosylated glycan pattern similar to that found on human
CC neutrophils and monocytes. Murine cells expressing human Fuc-TIV
CC show enhanced adhesion to E-selectin fusion proteins, indicating
CC that Fuc-TIV is involved in human granulocyte extravasation. Host
CC cells (e.g. 32D c13 or human 293 cells) transformed with DNA (see
CC also AAT59506) encoding Fuc-TIV and DNA encoding murine alpha-(1,3)-
CC fucosyltransferase (see also AAW11820), can be used to fucosylate
CC ADP-antibody, IgG or IgM for use in protecting an animal against an
CC adverse immune reaction, esp. septic shock or septicaemia.
XX
XX Sequence 405 AA;
XX
XX Query Match 34.6%; Score 681.5; DB 18; Length 405;
XX Best Local Similarity 38.0%; Pred. No. 2.4e-53;
XX Matches 151; Conservative 61; Mismatches 110; Indels 75; Gaps 14;
XX
XX QY 15 VCIIILGCFMAC--LLIYI-----KPTNSWIFSPMESASSVLKMKNFSTKTDYFNETHILV 68
XX Db 28 VCVLAAAGLCTALITYACWGLPLPFWA-SPTPS-----RPGVLL 68
XX
XX QY 69 WVPFEGQTEDL---TSCQAMENIOGCHLTDRSLYNKSHAVLIHHRDI-----SW---- 115
XX Db 69 WVEPFGAISAPRPPDCLRFNLSGCRLLTDRASGEAQAFLFHHDLVKGPDPPWPPW 128
XX
XX QY 116 -----DLTNLPQO-----ARPPFKQIWMNLESPTHTP-QKSGIEHL 151
XX Db 129 GIOHTAEVDLRLDYEEAAAAAALATSSPRPRAKRWYMMNFESPSHGLRSLASNL 188
XX
XX QY 152 FNLTLTYRRSDIQVYGFIVTSTNPEVFEVS-----KELVCWVYVSNWNPHEARV 203
XX Db 189 FNNWLSYRADSDVFVPGYLYPRSH--GDPPSGLAPPLSRKQGLVAWVYVSHWDERQARV 246
XX
XX QY 204 KYNELSKSIEHTYGOAF-GEVYNDKNLPTISACKFYLSFENSIIHKDYITEKLY-NAF 261
XX Db 247 RYTHQLSQHTVDVFGGCGQVPELGLLHTVARYKFYLAFENSQHLDIYITEKLMKNAL 306
XX
XX QY 262 LAGSVPVVLGPSRENYENIPADSFTHVEDYNSPSELAKYLKEVDKKNKLYLSFYFNWRKD 321
XX Db 307 LAGAVPVVLGPDRAHYERFVPRGAFIHVDVDFPSASSLASLYLLFLDRNPAYRYRFFHWR 366
XX
XX QY 322 FTVNLPWFESHACLADHVKRHOEY-KSVGNLEKWF 357
XX Db 367 YAVHITSFDEPWCRCQAVQVRAGDRPKSRNLASWF 403
XX
XX RESULT 11
XX AAW14515
XX ID AAW14515 standard; Protein; 360 AA.
XX
XX AC AAW14515;
XX
XX
```

```
DT 19-JUN-1997 (first entry)
XX
DE Human chimeric fucosyltransferase Fuc-TC4.
XX
KW Alpha(1,3/1,4)-fucosyltransferase; Lewis enzyme; Fuc-TIII;
KW alpha(1,3)-fucosyltransferase; Fuc-TVI; glycosylation;
KW oligosaccharide; Fuc-TC4.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Region 1..159
FT /label= Fuc-TIV
FT /note= "amino acids 1-159 of Fuc-TIV"
FT Region 160..360
FT /label= Fuc-TIII
FT /note= "amino acids 161-361 of Fuc-TIII"
FT Modified-site 46
FT /label= Glycosylation
FT Modified-site 91
FT /label= Glycosylation
FT Modified-site 153
FT /label= Glycosylation
XX
XX WO9709421-A1.
XX
XX 13-MAR-1997.
XX
XX 06-SEP-1996; 96WO-US13816.
XX
XX 08-SEP-1995; 95US-0525058.
XX
XX (UNMI ) UNIV MICHIGAN.
XX
XX Legault DJ, Lowe JB;
XX WPI: 1997-192897/17.
XX
XX New recombinant fucosyltransferase proteins - useful for modifying
XX cell surface oligosaccharide structures
XX
XX Claim 1; Refer to Page 294; 329pp; English.
XX
XX Chimeric fucosyltransferases Fuc-TC1 to Fuc-TC21 (AAW14512-31)
XX comprise portions of the human GDP-Fuc:(beta-D-Gal(1,4/1,3))-D-
XX GlcNAc(Glc) alpha(1,3/1,4)-fucosyltransferase (Fuc-TIII, Lewis
XX enzyme) (AAW13638) and portions of the GDP-Fuc:beta-D-Gal(1,4)-D-
XX GlcNAc alpha(1,3)fucosyltransferase (Fuc-TVI) (AAW13643). They are
XX obtd. by cassette mutagenesis of Fuc-TIII and Fuc-TVI nucleic acids
XX (AAT61675, AAT61680) and expression in transformed host cells. The
XX chimeric fucosyltransferases can be used to modify cell surface
XX oligosaccharide structures.
XX
XX Sequence 360 AA;
XX
XX Query Match 34.3%; Score 676; DB 18; Length 360;
XX Best Local Similarity 42.8%; Pred. No. 6.3e-53;
XX Matches 133; Conservative 62; Mismatches 104; Indels 12; Gaps 8;
XX
XX QY 55 STDTYFNETHILVWVWPGQTEDLTSCQAMF-NIOGCHLTDRSLYNKSHAVLIHHRDI 113
XX Db 53 STGTPAHISIPILLIWLWTFNFKPIALPCSEMPGTADCNITADRKVPQADAVIHIREV 112
XX
XX QY 114-SWD-LTNLPQOARPPFKQIWMNLESPTHTPQKSGIEHLFNLTLTYRRSDIQVYGFILT 172
XX Db 113 MYNPSAQLPSRPRQGRWIWFSMESPSHCWQLKAMDGYENLTMYSRSDSDITTPYGLW 172
XX
XX QY 173 V-STNPF--VFEVPSKEKLVCVWVYVSNWNPHEARVKKYNNELSKSIEHTYGOAFGEYVNDK 229
XX Db 173 PWSGQAPHPPLNLNAKTELVAWVSNWNPDSARVRYQSLQAHLKVDVYGRSH-KLPLKG 231
XX
XX QY 230 NLIPTISACKFYLSFENSIIHKDYITEKLY-NAFLASGVVVLGPSRENYENIPADSFIIH 288
XX
```

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Db 232 TMMETLSRYKFYLAENSLHPDYITEKLRNALAEAWAVPVVGLGPKSRNRYERFLPPDAFIH 291
QY 289 VEDYNSPSELAKYLKEVDKNNKLYLSYFNWRKDFTVNLPR--FWESHACACLDHVKRHOE 346
Db 292 VDDFQSPKDLARYLQELDKDHARYLSYFRWRETLR---PRFSWALDFCKACWKLQESR 348
QY 347 YKSVGNLEKWF 357
Db 349 YQTVRSIAAWF 359

RESULT 12
AAW14514
ID AAW14514 standard; Protein; 360 AA.
AC AAW14514;
XX
DT 19-JUN-1997 (first entry)
DE Human chimeric fucosyltransferase Fuc-TC3.
XX
KW Alpha(1,3/1,4)-fucosyltransferase; Lewis enzyme; Fuc-TIII;
KW alpha(1,3)-fucosyltransferase; Fuc-TVI; glycosylation;
KW oligosaccharide; Fuc-TC3.
XX
OS Synthetic.
XX
FH Key
FH Region 1..300
FT /label= Fuc-TIV
FT /note= "amino acids 1-300 of Fuc-TIV"
FT
FT Region 301..360
FT /label= Fuc-TIII
FT /note= "amino acids 302-361 of Fuc-TIII"
FT
FT Modified-site 46
FT /label= Glycosylation
FT
FT Modified-site 91
FT /label= Glycosylation
FT
FT Modified-site 153
FT /label= Glycosylation
FT
XX WO9709421-AL.
PN 13-MAR-1997.
XX
XX 06-SEP-1996; 96WO-US13816.
XX
XX 08-SEP-1995; 95US-0525058.
XX
XX (UNMI ) UNIV MICHIGAN.
XX
XX Legault DJ, Lowe JB;
XX
XX WPI; 1997-192897/17.
XX
XX New recombinant fucosyltransferase proteins - useful for modifying
XX cell surface oligosaccharide structures
XX
XX Claim 1; Refer to Page 294; 329pp; English.
XX
XX Chimeric fucosyltransferases Fuc-TC1 to Fuc-TC21 (AAW14512-31)
XX comprise portions of the human GDP-Fuc:(beta-D-Gal(1,4/1,3))-D-
XX GlcNAc(GlcNAc alpha(1,3/1,4)-fucosyltransferase (Fuc-TIII, Lewis
XX enzyme) (AAW13638) and portions of the GDP-Fuc:beta-D-Gal(1,4)-D-
XX GlcNAc alpha(1,3)fucosyltransferase (Fuc-TVI) (AAW13643). They are
XX obcd. by cassette mutagenesis of Fuc-TIII and Fuc-TVI nucleic acids
XX (AAW16175, AAW16180) and expression in transformed host cells. The
XX chimeric fucosyltransferases can be used to modify cell surface
XX oligosaccharide structures.
XX
XX Sequence 360 AA;

```

Query Match

34.3%; Score 675; DB 18; Length 360;

```

Best Local Similarity 42.8%; Pred. No. 7.8e-53;
Matches 133; Conservative
QY 55 STKTDYFNEITILVWVPFGOTFDLTSCQAMF-NIOGCHLTTRDSLYNKSHAVLIHHRDI 113
Db 53 STGTPAHISIPILLLWTFNFKPIALPRCSEMVPGTACDNITADRKVYPQADAVIVHREV 112
QY 114 SWD-LTNLPQOARPPFKWIWMNLESTHTPQKSGIEHLNLTLYRRDSIQVPGFLT 172
Db 113 MYNPSAQLPRSPRQGRWIWFSMESPSHCWQLKAMDGYFNLTMSYRSDSDITFTYGWLE 172
QY 173 V-STNPF--VFEVPSKEKLYCVVSVNNWNPHEARVYKYYNELSKSIEHTHYGOAFGEYVNDK 229
Db 173 PWSGQPAHPPLNLISAKTELVAWAVSNMGPNRSARVYYQSLQAHLKVDVYGRSH-KPLPQG 231
QY 230 NLIPTISACKFYLSFENSIIHKDYITEKLY-NAFLAGSVPVVGLGPKSRNRYENYIPADSFIIH 288
Db 232 TMMETLSRYKFYLAENSLHPDYITEKLRNALAEAWAVPVVGLGPKSRNRYERFLPPDAFIH 291
QY 289 VEDYNSPSELAKYLKEVDKNNKLYLSYFNWRKDFTVNLPR--FWESHACACLDHVKRHOE 346
Db 292 VDDFQSPKDLARYLQELDKDHARYLSYFRWRETLR---PRFSWALDFCKACWKLQESR 348
QY 347 YKSVGNLEKWF 357
Db 349 YQTVRSIAAWF 359

RESULT 13
AAW14530
ID AAW14530 standard; Protein; 361 AA.
XX
XX AAW14530;
XX
DT 19-JUN-1997 (first entry)
DE Human chimeric fucosyltransferase Fuc-TC19.
XX
KW Alpha(1,3/1,4)-fucosyltransferase; Lewis enzyme; Fuc-TIII;
KW alpha(1,3)-fucosyltransferase; Fuc-TVI; glycosylation;
KW oligosaccharide; Fuc-TC19.
XX
OS Synthetic.
XX
FH Key
FH Region 1..99
FT /label= Fuc-TIII
FT /note= "amino acids 1-99 of Fuc-TIII"
FT
FT Region 100..160
FT /label= Fuc-TVI
FT /note= "amino acids 99-159 of Fuc-TVI"
FT
FT Region 161..361
FT /label= Fuc-TIII
FT /note= "amino acids 161-361 of Fuc-TIII"
FT
FT Modified-site 154
FT /label= Glycosylation
XX
XX WO9709421-AL.
XX
XX 13-MAR-1997.
XX
XX 06-SEP-1996; 96WO-US13816.
XX
XX 08-SEP-1995; 95US-0525058.
XX
XX (UNMI ) UNIV MICHIGAN.
XX
XX Legault DJ, Lowe JB;
XX
XX WPI; 1997-192897/17.
XX
XX New recombinant fucosyltransferase proteins - useful for modifying
XX cell surface oligosaccharide structures

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OM protein - protein search, using sw model

Run on: October 8, 2002, 16:34:47 ; Search time 15.5 Seconds
(without alignments)
2225.553 Million cell updates/sec

Title: US-09-744-748-2
Perfect score: 1970
Sequence: 1 MPTSTGILRPFLIVCIILG.....HVKRHQYKSVGNLEKWFVN 359

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 71.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	703	35.7	433	2 A57596	alpha-1,3-fucosyl
2	695	35.3	400	2 JC4591	alpha-1,3 fucosyl
3	689.5	35.0	405	2 B36340	alpha(1,3)-fucosyl
4	667	33.9	361	2 A36669	galactoside 3(4)-L
5	667	33.9	374	2 A42270	alpha (1,3) fucosyl
6	662.5	33.6	359	2 A45156	alpha-(1,3)-fucosyl
7	653	33.1	365	2 S53498	alpha(1,3/4)-fucosyl
8	647	32.8	364	2 I39048	alpha (1,3) fucosyl
9	619	31.4	342	2 A54057	alpha(1,3) fucosyl
10	478.5	24.3	304	2 I39049	alpha (1,3) fucosyl
11	311	15.8	414	2 T15270	hypothetical prote
12	308	15.6	1652	2 T16799	hypothetical prote
13	281.5	14.3	451	2 T23491	hypothetical prote
14	224.5	11.4	393	2 H96742	hypothetical prote
15	203.5	10.3	513	2 F96533	probable fucosyltr
16	160.5	8.1	183	2 C97832	alpha-(1,3)-fucosyl
17	151.5	7.7	346	2 T44327	hypothetical prote
18	131	6.6	436	2 G71862	alpha-(1,3)-fucosyl
19	129.5	6.6	425	2 C64567	fucosyltransferase
20	129	6.5	454	2 B71914	alpha (1,3)-fucosyl
21	128.5	6.5	476	2 C64601	fucosyltransferase
22	123.5	6.3	876	2 S71277	serine/threonine-s
23	123.5	6.3	876	2 D85350	hypothetical prote
24	112.5	5.7	682	2 F81332	probable periplasm
25	110	5.6	1088	2 T41671	hypothetical prote
26	105.5	5.4	789	2 G90587	lipoprotein [impor
27	105	5.3	537	2 T21823	hypothetical prote
28	103	5.2	747	2 T33488	hypothetical prote
29	102	5.2	2628	2 S59413	probable membrane

30	101.5	5.2	354	2 B97003	spermidine/putresc
31	101	5.1	4550	2 T18440	hypothetical prote
32	100.5	5.1	382	2 T29554	hypothetical prote
33	99.5	5.1	335	2 AD1880	hypothetical prote
34	99.5	5.1	759	2 I38593	fibroblast activat
35	99	5.0	526	2 F82873	hypothetical prote
36	98.5	5.0	781	1 Q08B7	helicase (EC 3.6.1
37	98	5.0	392	2 D64433	hypothetical prote
38	98	5.0	408	2 T47585	hypothetical prote
39	98	5.0	441	2 F84560	purple acid phosph
40	96	4.9	387	2 JC2484	xylan endo-1,3-bet
41	96	4.9	566	2 JH0218	cellulase (EC 3.2.
42	96	4.9	2059	2 T41933	large tegument pro
43	95.5	4.8	340	2 T46112	hypothetical prote
44	95.5	4.8	370	2 JC7591	spinal cord-derive
45	95.5	4.8	373	2 F81438	probable periplasm

ALIGNMENTS

RESULT 1

A57596
alpha-1,3-fucosyltransferase Fuc-TIV (EC 2.4.1.-) - mouse
N:Alternate names: ELAM-1 ligand fucosyltransferase homolog
C:Species: Mus musculus (house mouse)
C:Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 11-Jan-2000
C:Accession: A57596
R:Gersten, K.M.; Natsuka, S.; Trinchera, M.; Petryniak, B.; Kelly, R.J.; Hiraiwa, N.,
J. Biol. Chem. 270, 25047-25056, 1995
A:Title: Molecular cloning, expression, chromosomal assignment, and tissue-specific e
rase.
A:Reference number: A57596; MUID:96027607
A:Accession: A57596
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-433 <R>
A:Cross-references: GB:033457; NID:gl039426; PIDN:AAC52269.1; PID:gl039427
C:Superfamily: galactoside 3(4)-L-fucosyltransferase
C:Keywords: glycosyltransferase; hexosyltransferase

Query Match	35.7%	Score	703;	DB	2;	Length	433;
Best Local Similarity	42.4%	Pred. No.	4.9e-46;				
Matches	145;	Conservative	49;	Mismatches	96;	Indels	52;
Gaps	8;						
QY	66	ILVWVWPF----	GQTDLTSCQAMFNIGQCHLTDRSLYKSHAVLIHHRDISMDLTNLP	121			
Db	92	VLLWVEFGRGGYKPKSPDCLSRFNISGCRLLTDRAAYGEAQAVLFHRLDKELHWP	151				
QY	122	QQ-----	-----ARPPFQKWMNLESPTHTPKSG	147			
Db	152	PMGARETDKALVLRVDDQEGAVTLTGKALETVGSRPGQVRWWMNFESPSHTPLRG	211				
QY	148	I--EHLPLTLTYRDSIDQVPGFLTVSTNPFPVEPS-----	KEKLCVWVSNWP	198			
Db	212	LAKDLFWNTLSYRDSVDFVPGFLYSRSP--TEQPSGLGPQLARRGLVWVWVSNWNE	269				
QY	199	EHARKYNNELSKSIEHTYQQAQF-GEYVNDKNLIPTISACKFYLSFENSITKDYIEKL	257				
Db	270	HQARVRYHQLSRHVSVDVGRGTGPRVPAIGLLHTVARYKYFLAFENSRHVDYIEKL	329				
QY	258	Y-NAFLAGSPVVLGSPRENYIIPADSIHVEDYNSPSELAKYLKEVDKNNKLYSYF	316				
Db	330	WRNAFLAGAPVVLGPDPRANYERFVPRGAFIHVDDDFNAASLAAYLLFLDRNVAVRYRF	389				
QY	317	NWRKDFTVNLPREWESHACLACDHVKRH--QEQKSVGNLEKWF	357				
Db	390	RWRRSFAVHITSFWDQWCRTCQAVQTSQDQPKSIHNLADWF	431				

RESULT 2

JC4591
alpha-1,3 fucosyltransferase (EC 2.4.1.-) - mouse

C:Species: Mus musculus (house mouse)
C:Date: 16-Apr-1996 #sequence_revision 24-May-1996 #text_change 24-Nov-1999
C:Accession: J04591
R:Ozawa, M.; Muramatsu, T.
J. Biochem. 119, 302-308, 1996
A:Title: Molecular cloning and expression of a mouse alpha-1,3 fucosyltransferase gene
A:Reference number: J04591; MUID:97037075
A:Accession: J04591
A:Molecule type: mRNA
A:Residues: 1-400 <OZ>
A:Cross-references: DBJ:D63379
A:Experimental source: Embryonal carcinoma F9 cells
C:Keywords: galactoside 3(4)-L-fucosyltransferase
C:Keywords: glycoprotein; glycosyltransferase; hexosyltransferase
F:1-23/Domain: intracellular #status predicted <INT>
F:24-49/Domain: transmembrane #status predicted <TRM>
F:84,185/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 35.3%; Score 695; DB 2; Length 400;
Best Local Similarity 41.8%; Pred. No. 1.8e-45;
Matches 143; Conservative 51; Mismatches 96; Indels 52; Gaps 8;

QY 66 ILVWVWP-----GQTFDLTSCQAMNIQCHLTDRSLYNKSHAVLIHHRDISWDLTNLP 121
DB 59 VLLWEPFGRGGYKSPDPSLRNISGCRLLTDRAAYGEAAQVLFHRLDLVKELHWP 118
QY 122 QQ-----ARPPQKWTMMLESPTHTPPQKSG 147
DB 119 PPMGARETDKALVLRVDDQEGAVTLGKALETVGSRPPGQRYWMMNFESPSTHPPGLRG 178
QY 148 I-EHLNLTATVRRSDIOVPYGLFTVSTNPFVFPVS-----KEKLVGVYVSNWNP 198
DB 179 LAKDLNFWTLSTYRSDVFPYGLYSRSDP--TEQPSGLGPPPLARKOGLEAWVYVSNWNE 236
QY 199 EHARKYNELSKSIEIHTYQAF-GEVYNDKNLIPTISACKFYLSFENSITHKDYITEKL 257
DB 237 HQAQVRYXHQLSHRVSDVFGRTGPRVPVPAIGLLHTVARYKFLAFENSRRHVDYITEKL 296
QY 258 Y-NAFLAGSVPVVLGSPRENYENIPADSFIVEDYNSPSELAKYLVKEVDKNNKLYLYSF 316
DB 297 WRNAFLAGVPPVVLGSPDRANYERFVPRGAFIHVDDEPNAASLAAYLLFLDRNAVYRYF 356
QY 317 NWRKDFTNLPRFWSHACLDHVKRH-QEYKSGVNLKWF 357
DB 357 RWRRSFAVHTSFWEQRCRTCAQVOTSGDQPKSHNLADWF 398

RESULT 3
B36340
alpha(1,3)-fucosyltransferase (EC 2.4.1.-) 4 precursor [validated] -- human
N:Alternate names: CD15; ELAM-1 ligand fucosyltransferase (ELFT); FCT3A; FUC-TIV; myeloid
C:Species: Homo sapiens (man)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: B36340; A36340; A40976; A41202
R:Goelz, S.E.; Hession, C.; Goff, D.; Griffiths, B.; Tizard, R.; Newman, B.; Chi-Rosso,
Cell 63, 1349-1356, 1990
A:Title: ELFT: a gene that directs the expression of an ELAM-1 ligand.
A:Reference number: A36340; MUID:91084863
A:Accession: B36340
A:Molecule type: mRNA
A:Residues: 1-405 <GOE1>
A:Cross-references: GB:M58596; NID:g182068; PIDN:AAA63172.1; PID:g182069
A:Accession: A36340
A:Molecule type: mRNA
A:Residues: 'MRLWGAARKPSGAGWEKAEAPQAPGWSGRGLPGK', 'SGRKGRAVPQWASWPAHLAARPARHLGGAG
A:Cross-references: GB:M58597; NID:g182070; PIDN:AAA63173.1; PID:g182071
A>Note: the codon used as an initiator for this translation is not in a good context for
R:Low, J.B.; Kukowska-Latallo, J.F.; Nair, R.P.; Larsen, R.D.; Marks, R.M.; Macher, B.A.
J. Biol. Chem. 266, 17467-17477, 1991
A:Title: Molecular cloning of a human fucosyltransferase gene that determines expression
A:Reference number: A40976; MUID:91373370
A:Accession: A40976
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-86, 'P', 88-405 <LOW>
A:Cross-references: GB:M65030; NID:g182791; PIDN:AAA92977.1; PID:g1236720
R:Kumar, R.; Potvin, B.; Muller, W.A.; Stanley, P.
J. Biol. Chem. 266, 21777-21783, 1991
A:Title: Cloning of a human alpha(1,3)-fucosyltransferase gene that encodes ELFT but
A:Reference number: A41202; MUID:92042084
A:Accession: A41202
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-240, 'D', 242-400 <KUD>
A:Cross-references: GB:S65161; NID:g239005; PIDN:AAB20349.1; PID:g239006
C:Genetics: GDB:FUT4; CD15; FCT3A; FUC-TIV
A:Cross-references: GDB:131563; OMIM:104230
A:Map position: 11q21-11q22
C:Superfamily: galactoside 3(4)-L-fucosyltransferase
C:Keywords: glycoprotein; glycosyltransferase; hexosyltransferase
F:1-48/Domain: signal sequence #status predicted <SIG>
F:49-405/Product: alpha(1,3)-fucosyltransferase 4 #status predicted <MAT>
F:91,190/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 35.0%; Score 689.5; DB 2; Length 405;
Best Local Similarity 38.5%; Pred. No. 4.8e-45;
Matches 153; Conservative 60; Mismatches 109; Indels 75; Gaps 14;

QY 15 VCIILGCFMAC--LLIYI---KPTNSWIFSPMESASSVLKMKNFSTTKTDYFNETTILV 68
DB 28 VCVLAAAGLCTALITYACNGQLPLPWA-SPTPS-----RPVGVLL 68
QY 69 WWVPFGQTFDL---TSCQAMFNTQCGHLLTDRSLYNKSHAVLIHHRDI-----SW---- 115
DB 69 WVEPFGGRDSAPRPPPCRLFRNISGCRLLTDRAAYGEAAQVLFHRLDLVKGPDPWPPW 128
QY 116 -----DLTNLPQO-----ARPPQKWTMMLESPTHTP-OESGIEHL 151
DB 129 GIOAHTAEVDLRLVDEEAAAAAALATSSPPRPGQRYWMMNFESPSPGLSLASNL 188
QY 152 FNLTATVRRSDIOVPYGLFTVSTNPFVFPVS-----KEKLVGVYVSNWNP 203
DB 189 FNWTLSEADSDVFPYGLYPSHP--GDPPSGLAPLSRKGGLVAVVSWHDERQAV 246
QY 204 KYNELSKSIEIHTYQAF-GEVYNDKNLIPTISACKFYLSFENSITHKDYITEKL 261
DB 247 RYHQLSQHVTVDFVGGGQCPVEIGLLHTVARYKFLAFENSQHLDYITEKLNRNAL 306
QY 262 LAGSVPVVLGSPRENYENIPADSFIVEDYNSPSELAKYLVKEVDKNNKLYLYSFNMRKD 321
DB 307 LAGAVPVVLGSPDRANYERFVPRGAFIHVDDEPNAASLAAYLLFLDRNPVYRYFHWRRS 366
QY 322 FTVNLPRFWSHACLDHVKRHQY-KSVGNLEKWF 357
DB 367 YAVHTSFWEQRCRTCAQVQVQAGDRPKSIRNLASWF 403

RESULT 4
A36669
galactoside 3(4)-L-fucosyltransferase (EC 2.4.1.65) -- human
N:Alternate names: alpha (1,3/1,4) fucosyltransferase; blood group Lewis alpha-4-fucc
C:Species: Homo sapiens (man)
C:Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 29-Sep-1999
C:Accession: A36669; I39043; I39045; I39045; S12123
R:Kukowska-Latallo, J.F.; Larsen, R.D.; Nair, R.P.; Lowe, J.B.
Genes Dev 4, 1288-1303, 1990
A:Title: A cloned human cDNA determines expression of a mouse stage-specific embryoni
A:Reference number: A36669; MUID:91032981
A:Accession: A36669
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-361 <KUK>
A:Cross-references: GB:M53578; NID:g28529; PIDN:CAA37641.1; PID:g28530
R:Cameron, H.S.; Szczepaniak, D.; Weston, B.W.
J. Biol. Chem. 270, 20112-20122, 1995

J. Biol. Chem. 270, 20112-20122, 1995
A;Title: Expression of human chromosome 19p alpha(1,3)-fucosyltransferase genes in non-human primates.
A;Reference number: I39043; MUID: 95378269

A;Accession: I39046
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <RES>
A:Cross-references: EMBL:U27329; NID:g967194; PIDN:AAC50188.1; PID:g967195
A:Accession: I39047
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <RE2>
A:Cross-references: EMBL:U27330; NID:g967196; PIDN:AAC50189.1; PID:g967197
C:Genetics:
A:Gene: GDB:FUT5
A:Cross-references: GDB:I31644; OMIM:I36835
A:Map position: 19p13.3-19p13.3
C:Superfamily: galactoside 3(4)-L-fucosyltransferase

Query Match 33.9%; Score 667; DB 2; Length 374;
Best Local Similarity 43.7%; Pred. No. 2.2e+43;
Matches 131; Conservative 58; Mismatches 99; Indels 12; Gaps 8;

Qy 66 ILVWVPFGQTFLDTSQAMP-NIQGCHLTDRSLYNKSHAVLIHHRDISWD-ITNLPPQQ 123
||| ||| | | : | : | : | : | : | : | : | :
Db 78 ILLTWPFNTPVALPRGSVMYPGAADCNITADSSVYPQDAIVVHHVDIMYNSANLPPP 137

Qy 124 ARPFEQKWMMNLESPTHTPQKSIEHLNLTLYRRDSIOVPYGFLT-V-STNP-F--VF 180
||| ||| : ||| : : ||| : ||| ||| ||| : |
Db 138 TRPGQRWIWFMSPNCRLEALOGYFNLTMYTRSDSIFTFYGNLPWSWGQAHPPL 197

Qy 181 EVPSKEKLVCVVSNWPENHARVKYYNELSKSIIBHTYGOAFGEYVNDKNLIPTISACKF 240
: ||| ||| ||| : ||| ||| : ||| : : : ||| : ||
Db 198 NLSAKTELVAWVSNNKPDSARVRYYSLOAHLKVDVYGRSH-KPLPKGTMTLSRVKF 256

Qy 241 YLSPEHSIHDKYTEKYL-NAFLAGSPVVLGPGRSENYENTIPADSFIHVEDYNSPELA 299
||| ||| : ||| ||| : ||| ||| ||| ||| : ||| ||| : ||| : ||
Db 257 YLAFENSILPDYITEKLRNALAEAWPVVLGPSRSNYERLPPDAETHVDFOFSKDLa 316

Qy 300 KYLEVKNKKLXSYFNWRKDETVNLP-R--FWESHACLACHVKRHOEYKSVGNLEKWF 357
:||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| : ||
Db 317 RYQLQDLKHARYLSYFRWRET LR---PRSFWALLAFCKACWKLOQESRYOTVRSIAAWF 373

RESULT 6
A45156
alpha-(1,3)-fucosyltransferase FUT6 - human
N;Alternate names: alpha-(1,3)-fucosyltransferase Fuc-TVI; fucosyltransferase 6; Lewis X
C;Species: Homo sapiens (man)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 29-Sep-1999
C;Accession: A45156; JCI1228; I39050; I39051; I39052; I39053; I39054
R;Weston, B.W.; Smith, P.L.; Kelly, R.J.; Lowe, J.B.
J. Biol. Chem. 267, 24575-24584, 1992
A;Title: Molecular cloning of a fourth member of a human alpha(1,3)fucosyltransferases
l sialyl Lewis x epitopes.
A;Reference number: A45156; MUID:93077550
A:Accession: A45156
A:Molecule type: DNA
A:Residues: 1-359 <WES>
A:Cross-references: GB:I01698; NID:g182792; PIDN:AAB03078.1; PID:g1280210
R;Koszidin, K.L.; Bowen, B.R.
Biochem. Biophys. Res. Commun. 187, 152-157, 1992
A;Title: The cloning and expression of a human alpha-1,3 fucosyltransferase capable of forming
A;Reference number: JCI1228; MUID:92392318
A:Accession: JCI1228
A:Molecule type: mRNA
A:Residues: 1-359 <KOS>
A:Cross-references: GB:M98825; NID:g182491; PIDN:AAA99222.1; PID:g182492
A;Note: the authors translated the codon GAC for residue 219 as Asn
R;Cameron, H.S.; Szczepaniak, D.; Weston, B.W.
J. Biol. Chem. 270, 20112-20122, 1995
A;Title: Expression of human chromosome 19p alpha(1,3)-fucosyltransferase genes in non-

A:Accession: I39050
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-359 <RES>
A:Cross-references: EMBL:U27333; NID:g967202; PIDN:AAC50192.1; PID:g967203
A:Accession: I39051
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-359 <RE2>
A:Cross-references: EMBL:U27334; NID:g967204; PIDN:AAC50193.1; PID:g967205
A:Accession: I39052
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-359 <RE3>
A:Cross-references: EMBL:U27335; NID:g967206; PIDN:AAC50194.1; PID:g967207
A:Accession: I39053
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-359 <RE4>
A:Cross-references: EMBL:U27336; NID:g967208; PIDN:AAC50195.1; PID:g967209
A:Accession: I39054
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-359 <RE5>
A:Cross-references: EMBL:U27337; NID:g967210; PIDN:AAC50196.1; PID:g967211
C:Genetics:
A:Gene: GDB:FUT6
A:Cross-references: GDB:I35180; OMIM:136836
A:Map position: 19p13.3-19p13.3
C:Superfamily: galactoside 3(4)-L-fucosyltransferase
C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 33.6%; Score 662.5; DB 2; Length 359;
Best Local Similarity 42.8%; Pred. No. 4.6e-43;
Matches 133; Conservative 59; Mismatches 106; Indels 13; Gaps 9;

QY 55 STKTDYFNETTILVWVWPFQGTDLTSCQAMF-NIOGCHLTDRSLYNKSHAVLIHHRDI 113
DB 53 STGTPAHSIPLILLWTFPNKPIALPRCSSEMPVGTADCNITADRKVPQADAVIVHREV 112

QY 114 SWD-LTNLPQARPPPKWIMNLESHTHTPKSGIEHLNLTITRSDSDIYVPYGLT 172
DB 113 MINPSAQLPRPQGGQWIFWFSMESHCWQLKAMDGYFNLMTYSRSDSDIFTYPYGLWLE 172

QY 173 V-STNPF--VFEVPSKEKLVWVWVNNPEHARVKYINELSKSIEHTYGOAFGEYVNDK 229
DB 173 FWSGQPAHPPNLNLSAKTELVAWVWVNNPEHARVKYINELSKSIEHTYGOAFGEYVNDK 231

QY 230 NLIPTISACKFYLSPFNSIHADYITEKLY-NAFLAGSVVPVVLGSPRENYENYIPADSFH 288
DB 232 TMETLSRYKFLAFENSLHPDYITEKLRNLALEAWVPPVVLGSPRSNYERFLPPDAFIH 291

QY 289 VEDYNPSSELAKEYLKEVDKNNKLYLSYFNWRKDFTNLPR--FWESHACIACDHYKRRHQE 346
DB 292 VDDFQSPKDLARYLQELDKHARVLSYFRWRETLR---PRSFWSALAFCKACWKLOQESR 348

QY 347 YKSVGNLEKWF 357
DB 349 YQTRG-IAAWF 358

RESULT 7
S55498
alpha(1,3/4)-fucosyltransferase - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 13-Sep-1998
C:Accession: S55498
R:Oulmouden, A.; Wierinkx, A.; Petit, J.M.; Julien, R.
submitted to the EMBL Data Library, June 1995
A:Description: Molecular cloning and expression of bovine alpha (1.3/4)-fucosyltransferase
A:Reference number: S55498
A:Accession: S55498
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-365 <OUL>
A:Cross-references: EMBL:X87810; NID:g860807; PID:g860808
C:Superfamily: galactoside 3(4)-L-fucosyltransferase

Query Match 33.1%; Score 653; DB 2; Length 365;
Best Local Similarity 38.3%; Pred. No. 2.5e-42;
Matches 141; Conservative 68; Mismatches 117; Indels 42; Gaps 12;

QY 11 PELIVCIIIG-CFMACILII--YIKPTNSWI-----FSPMESASSVLKMKNFSTKTDY 60
DB 18 PGLLLQLLLALCFPSYLRMSQEKPKPMWVSELGAPSOATEGSSAHLPLR----- 68

QY 61 FNETTILVWVWPGQGTDLTSCQAMF-NIOGCHLTDRSLYNKSHAVLIHHRDISW-DLT 118
DB 69 -----VLLTWPFNPQVALSCELMPGTADCOLTVNRSEYPOADAVFVHHRVSHRPM 123

QY 119 NLPOQARPPPKWIMNLESHTHTPKSGIEHLNLTITRSDSDIYVPYGLT-----T 172
DB 124 QLPSPRPADQQRWVWFSMESPSNCLKLDGYNFTMTSYRRSDIFMPYGMLEPWSPQ 183

QY 173 VSTNPFVFEVPSKEKLVWVWVNNPEHARVKYINELSKSIEHTYGOAFGEYVNDKNI 232
DB 184 VET---LLNLISAKTKLVAVVWVWVNNPDSIRVQYKLLKPHLQVDVYGR-FHTPLPHALMA 239

QY 233 PTISACKFYLSPFNSIHADYITEKLY-NAFLAGSVVPVVLGSPRENYENYIPADSFHVED 291
DB 240 KQLSQYKFLAFENSLHPDYITEKLRNLALEAWVPPVVLGSPRSNYERFLPPDAFIHVED 299

QY 292 YNPSSELAKEYLKEVDKNNKLYLSYFNWRKDFTNLPR--FWESHACIACDHYKRRHQEYS 349
DB 300 FQSPKDLAQYLLALDKDYASYLNLYFRWRETLR---PRSFWSALAFCKACWKLOQEPYQT 356

QY 350 VGNLEKWF 357
DB 357 VPSIASWF 364

RESULT 8
I39048
alpha(1,3) fucosyltransferase FUT6-related splice form I - human
C:Species: Homo sapiens (man)
C:Date: 01-Mar-1996 #sequence_revision 01-Mar-1996 #text_change 29-Sep-1999
C:Accession: I39048
R:Cameron, H.S.; Szczepaniak, D.; Weston, B.W.
J. Biol. Chem. 270, 20112-20122, 1995
A:Title: Expression of human chromosome 19p alpha(1,3)-fucosyltransferase genes in no
A:Reference number: I39043; MUID:95378269
A:Accession: I39048
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-364 <RES>
A:Cross-references: EMBL:U27331; NID:g967198; PIDN:AAC50190.1; PID:g967199
C:Genetics:
A:Gene: GDB:FUT6
A:Cross-references: GDB:I35180; OMIM:136836
A:Map position: 19p13.3-19p13.3
C:Superfamily: galactoside 3(4)-L-fucosyltransferase
C:Keywords: alternative splicing

Query Match 32.8%; Score 647; DB 2; Length 364;
Best Local Similarity 44.2%; Pred. No. 7.2e-42;
Matches 129; Conservative 54; Mismatches 97; Indels 12; Gaps 8;

QY 55 STKTDYFNETTILVWVWPGQGTDLTSCQAMF-NIOGCHLTDRSLYNKSHAVLIHHRDI 113
DB 53 STGTPAHSIPLILLWTFPNKPIALPRCSSEMPVGTADCNITADRKVPQADAVIVHREV 112

QY 114 SWD-LTNLPQARPPPKWIMNLESHTHTPKSGIEHLNLTITRSDSDIYVPYGLT 172
DB 113 MYNSAQLPRPQGGQWIFWFSMESHCWQLKAMDGYFNLMTYSRSDSDIFTYPYGLWLE 172

QY 173 V-STNPF--VFEVPSKEKLVWVWVNNPEHARVKYINELSKSIEHTYGOAFGEYVNDK 229

Db 173 PWSQPAHPPLNLGSAKTELVAWVSNWGNPSARVRYTQSLQAHKLVGVYGRSH-KPLPQG 231
Qy 230 NLIPTISACKFYLSPFENSIHKDYITEKLY-NAFLAGSVVPLGSPSRENYENIIPADSFIIH 288
Db 232 TMMETLSRYKFLAFENSLHPDYITEKLWRNLALEAWAVPVVLGSPSRNRYERFLPPDAFIIH 291
Qy 289 VEDYNSPSELAKYILKEVDKNNKLYLSPFNWRKDTVNLPR--FWESHACIAC 338
Db 292 VDFQSPKDLARYQLQELDKHARYLSYFRWRETLR---PRSFSAALAFCKAC 340

RESULT 9
A54057
alpha(1,3)-fucosyltransferase (EC 2.4.1.1) 7 precursor - human
N;Alternate names: leukocyte fucosyltransferase FucTVII
C;Species: Homo sapiens (man)
C;Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 20-Apr-2000
C;Accession: A54057; MUID:94237894
R;Sasaki, K.; Kurata, K.; Funayama, K.; Nagata, M.; Watanabe, E.; Ohta, S.; Hanai, N.; J. Biol. Chem. 269, 14730-14737, 1994
A;Title: Expression cloning of a novel alpha(1,3)-fucosyltransferase that is involved in b
A;Reference number: A54057; MUID:94237894
A;Accession: A54057
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-342 <SAS>
A;Cross-references: GB:X78031; NID:g516292; PIDN:CAA54962.1; PID:g516293
R;Natsuka, S.; Gersten, K.M.; Zenita, K.; Kannagi, R.; Lowe, J.B. J. Biol. Chem. 269, 16789-16794, 1994
A;Title: Molecular cloning of a cDNA encoding a novel human leukocyte alpha-1,3-fucosyl
A;Reference number: A53713; MUID:94266898
A;Accession: A53713
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-160, 'A', 163-303, 'SV', 306-342 <NAT>
A;Cross-references: GB:U08112; NID:g520463; PIDN:AAA56869.1; PID:g520464
C;Genetics:
A;Gene: GDB:FUT6
A;Cross-references: GDB:373982
A;Map position: 9pter-9qter
C;Superfamily: galactoside 3(4)-L-fucosyltransferase
C;Keywords: glycoprotein; glycosyltransferase; hexosyltransferase
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-342/Product: alpha(1,3)-fucosyltransferase 7 #status predicted <MAT>
F;81,291/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 31.4%; Score 619; DB 2; Length 342;
Best Local Similarity 43.0%; Pred. No. 9.1e-40;
Matches 129; Conservative 49; Mismatches 108; Indels 14; Gaps 8;

Qy 65 TILVWVWPF-GQTFDLTS--CQAMFNIQGCCHLTDRSLYNKSHAVLIHHRDISWDLTNLP 121
Db 48 TILVWHPFTDQPELPSDTC-TRYGIARCHLSANRSLASADAVVFRHRLQTRRSLP 106
Qy 122 QOAPPPQKWLMNLESPTHTPQSGIEHLFNLTTRDSDIQVPYGLTVSNPFFVE 181
Db 107 LAQPRGQPMWVWMSPESTHTGSLHGIENWVLSYRDRSDIFVYGRLEPHMGSP-P 165
Qy 182 VPSKEKLVWVSNWNPHEARVKNYELSKSIEIHTYGOAFGEYVNDKNLPTISACKFY 241
Db 166 LPAKSRVAWVVSFOERQLRARLYRQLAPHLRVDFVGRNGRPLCASCPLTVTAQYRFY 225
Qy 242 LSFENSIHKDYITEKLY-NAFLAGSVVPLGSPSRENYENIIPADSFIIHVEDYNSPSELAK 300
Db 236 LSFENSQHRDYITEKFWRNALVAGTPVPLGPPRATYEAFFADAFVHVDDFGSARELAA 285
Qy 301 YLKEVDKNNKLYLSPFNWRKDTVNLPRFWESHACIACD---HVKRHOEYKSVGNLEKWF 357
Db 286 FL--TGMNESYQRFARWRDLRVLEFDWREERFCAICDRYPHLPRSOVYE---DLEGWF 340

RESULT 10

I39049
alpha(1,3)-fucosyltransferase FUT6-related splice form II - human
C;Species: Homo sapiens (man)
C;Date: 01-Mar-1996 #sequence_revision 01-Mar-1996 #text_change 29-Sep-1999
C;Accession: I39049
R;Cameron, H.S.; Szczepaniak, D.; Weston, B.W. J. Biol. Chem. 270, 20112-20122, 1995
A;Title: Expression of human chromosome 19p alpha(1,3)-fucosyltransferase genes in m
A;Reference number: I39043; MUID:95378269
A;Accession: I39049
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-304 <RES>
A;Cross-references: EMBL:U27332; NID:g967200; PIDN:AAC50191.1; PID:g967201
C;Genetics:
A;Gene: GDB:FUT6
A;Cross-references: GDB:135180; OMIM:136836
A;Map position: 19p13.3-19p13.3
C;Superfamily: galactoside 3(4)-L-fucosyltransferase
C;Keywords: alternative splicing

Query Match 24.3%; Score 478.5; DB 2; Length 304;
Best Local Similarity 43.0%; Pred. No. 4.1e-29;
Matches 98; Conservative 42; Mismatches 81; Indels 7; Gaps 6;

Qy 55 STKTDYFNETTILVWVWPFQTFDLTSCQAMP-NIQGCHLTDRSLYNKSHAVLIHHRDI 113
Db 53 STGTPAHSLIPLILLWTWPFNKPIALPRCSEMVPGTADCNITADRKVYPQADAVIVHREV 112
Qy 114 SWD-LTNLPQOARPPQKWIWNLESPTHTPQSGIEHLFNLTLYRDRSDIQVPYGLTF 172
Db 113 MYNSAQLPRSPRQOGKRWIMFMSHSCWOLKAMDGYFNLTWYSRSDSDIFTYGWLE 172
Qy 173 V-STNPF--VEEVPSEKLVWVSNWNPHEARVKNYELSKSIEIHTYGOAFGEYVNDK 229
Db 173 PWSQPAHPPLNLGSAKTELVAWVSNWGNPSARVRYTQSLQAHKLVGVYGRSH-KPLPQG 231
Qy 230 NLIPTISACKFYLSPFENSIHKDYITEKLY-NAFLAGSVVPLGSPSREN 276
Db 232 TMMETLSRYKFLAFENSLHPDYITEKLWRNLALEAWAVPVVLGSPSRN 279

RESULT 11
TI5270
hypothetical protein F59E12.13 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Mar-2000
C;Accession: TI5270
R;Johnson, D. submitted to the EMBL Data Library, May 1997
A;Description: The sequence of C. elegans cosmid F59E12.
A;Reference number: Z18318
A;Accession: TI5270
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-414 <JOH>
A;Cross-references: EMBL:AF003386; NID:g2088833; PID:g2088845; PIDN:AAB54261.1; GSPD3
A;Experimental source: strain Bristol N2; clone F59E12
C;Genetics:
A;Gene: CESP:F59E12.13
A;Map position: 2
A;Local Similarity 28.0%; Pred. No. 3.8e-16;
Matches 98; Conservative 58; Mismatches 120; Indels 74; Gaps 17;

Query Match 15.8%; Score 311; DB 2; Length 414;
Best Local Similarity 28.0%; Pred. No. 3.8e-16;
Matches 98; Conservative 58; Mismatches 120; Indels 74; Gaps 17;

Qy 66 ILVWVWPFQTFD---LTSQAMFNIQGCCHLTDRSLYNKSHAVLIHHRDISWDLTNLP- 121
Db 67 ILYWTITFGATVPSTALSDCPGL--TDRCVITDRHQLDSADAVVFFHAADIS----KEPL 120
Qy 122 QOAPPPQKWLMNLESPTHTPQSG---IEHLFNLTLYRDRSD 163

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A:Reference number: Z19747
A:Accession: T23491
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-451 >KWL>
A:Cross-references: EMBL:Z66497; PIDN:CAA91285.1; GSPDB:GN00020; CESP:K08F8.3
A:Experimental source: clone K08F8
C:Genetics:
A:Gene: CESP:K08F8.3
A:Map position: 2
A:Antisense: 30/2; 53/3; 133/1; 195/3; 242/3; 277/3; 307/2; 342/3; 382/2
Query Match 14.3%; Score 281.5; DB 2; Length 451;
Best Local Similarity 30.1%; Pred. No. 7.7e-14;
Matches 86; Conservative 44; Mismatches 99; Indels 57; Gaps 1
QY 67 LVMVWPFQGTDLTSCQAMFNIGQ-----CHLTIDRSLYNKSHAVLIHHRDISWDLTNLP 121
DB 137 LILSNMAGHSQD-----NLQGGPDWNCFTQVRARAPADADAVLIAHMDNDF---VP 184
QY 122 QOARPPFOKWIWNWLESPTHTPKSGIE---HLENLTITLYRRSDIQVPYGFGL----- 171
DB 185 K---PNQVVVYFSQESPAN---SGIQIPREDYINMTLGFRRDTPAGSPGYGTVKLGAK 236
QY 172 -----TVSTNPFVPEVPSKEKLVGVVSNWNPENHARVKNYNNELSKSIEIHTYQG---- 220
DB 237 SRKTGOVDAN---LVNKGAKGAWFVSHICOTNSKREDFVKLQRLHQIDIYGGCGPMK 292
QY 221 -AFGEVNDKNLPIISACKFYLSPENSIIKHDIITEKLYNAELAGS-VPVILGSPRENYE 278
DB 293 CARGOSKCDTML---DTHYHFTVTFENSICEDYIVTEKLMKSGYQNTIPLVL--RKILVE 347
QY 279 NTPADSFTHEDVNSPELAKYKEVDKNKLYLSYFNWRKDFTV 324
DB 348 PFVPPNSFTADDFKSVKEMGDYLNLMNNKTAYMEYFEWRHDYKV 393
RESULT 14
H96742
hypothetical protein Fl7M19.14 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: H96742
R:R/Theologian, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, C.;
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Cressy, T.H.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin,
A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luo, J.S.; Maiti, R.;
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.;
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: H96742
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-393 <STO>
A:Cross-references: GB:AE005173; NTD:96978923; PIDN:AAF34315.1; GSPDB:GN00141
C:Genetics:
A:Gene: Fl7M19.14
A:Map position: 1
Query Match 11.4%; Score 224.5; DB 2; Length 393;
Best Local Similarity 26.2%; Pred. No. 1.4e-09;
Matches 90; Conservative 47; Mismatches 129; Indels 77; Gaps 1
QY 39 SPMESASSVLKMKNFSTKDYFNETTILV--WVPFGQTDLTSCQAMFNIGCHLTTD 96
DB 82 SLQEFQCGCKLKKH-----VKVLVGWTWIPNLNENLYSCR-----CGMT-- 121
QY 97 RSLYKNSHAVLIHHRDISWDLTNLPQOARPPFOKWIWNWLESPTHTPKOSGIEHFLNLT 156

```

Db 122 -CLWTKSSVLADSPDALLFETTTPLQRRVGDPLRVYMELEAGR---KRSREDIF---I 174
QY 157 TYRSDIQVYGFGLTVSTNPFVFEVPSK--EKLVCWVSVNWNPEHARVYKYNELSKS-- 212
Db 175 SYHAKDDVQTYAGSLFHNRRNHYHISPHKNDVLVYSSSRCLPHRDR-----LAKSL 228
QY 213 --IEIHTYGA-----FGEYNDKN-----LIPTISACKFYLSFENSIH 249
Db 229 DLIPHSFGKLNNGVGLDSALSMPYECVAEHAENAKWYDHLHCAMSHYKFLAIENTAV 288
QY 250 KDYTEKLYNAFLAGSVVPLVPSRENYENIPADGFIHVEDYNSPSELAKYLKEVDKN 309
Db 289 ESYVTEKLFALDVGSGVPIYFGAS--NVQFVPPHSHVSDGSKFGSMOELAAAYVKRLGDDP 346
QY 310 KLYLSYFNWR-----KDFVTNLPWFESHACLADHVKR 343
Db 347 VAYSEYHAWRRCLGMNGYKTRAVSL-----DTLPCRLEISR 385

RESULT 15
F96533
probable fucosyltransferase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: F96533
R:Rheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luross, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: F96533
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-513 <STO>
A:Cross-references: GB:AE005173; MID:g10120428; PIDN:AAG13053.1; GSPDB:GN00141
C:Genetics:
A:Gene: F14J22.8
A:Map position: 1

Query Match 10.3%; Score 203.5; DB 2; Length 513;
Best Local Similarity 25.7%; Pred. No. 8.3e-08;
Matches 77; Conservative 50; Mismatches 122; Indels 51; Gaps 15;
QY 56 TKTDYFNETHILVWVWPFQGFDTLSCQ---AMFNIGCH---LTDRSLYNKSHA---V 106
Db 70 TLTDFTQSPSL-----SOSPAPSRDKKIGLFTDRSCEWLMREDSVTSYRDTKDPI 123
QY 107 LIH--HRDISW---DLT-----NLPOQA---RPPQKWIWNLESPTHTPOKSGIEHL 151
Db 124 FISGGERDFQWCSVDCTFGSSCKTPDAAGLQKQKPTLSIIRSWESAQYPEN----- 177
QY 152 FNLTLYRSDSI-----QVPYGLTVSTNPFVFEV--PSKEKLYCWV--VSNWNPEHA 201
Db 178 -DLAQARRRGYDVMVTTSLSSDVPVGVFSNAEYDIMSVPQPKTERATAAFISNCGARNE 236
QY 202 RVXYYNELSK-STEIHTYGAQGEYVNDKNLIPTISACKFYLSFENSIHKDYITEKLYNA 260
Db 237 RLQALEALMTNKIDSYGCHNRDGVKVEALKRYKFSLAFENTNEEDYVTEKFFQS 296
QY 261 FLAGSVVWVLGSPRENYIPA--DSFIHVEDYNSPSELAKYLKEVDKNKLYLSYFNWR 319
Db 297 LVAGSVVPPVGP--PNIEEFAPASDSFLHKTHMEDVEPVAKRMKYLAAANPAAYNQTLRWK 354

Search completed: October 8, 2002, 16:54:37

Job time : 17.5 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 8, 2002, 15:06:57 ; Search time 8.5 Seconds
(without alignments)
(1635.332 Million cell updates/sec)

Title: US-09-744-748-2

Perfect score: 1970

Sequence: 1 WTSTSGILRPLIVCIILG.....HVKRHQYKSVGNLEKFWFN 359

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	703	35.7	433	1	FUT4_MOUSE
2	690.5	35.1	433	1	FUT4_MOUSE
3	687.5	34.9	405	1	FUT4_HUMAN
4	667	33.9	361	1	FUT3_HUMAN
5	667	33.9	374	1	FUT5_HUMAN
6	666	33.8	374	1	FUT5_PANTR
7	665	33.8	365	1	FUT3_BOVIN
8	662.5	33.6	359	1	FUT6_HUMAN
9	660	33.5	372	1	FUT3_PANTR
10	659.5	33.5	359	1	FUT6_PANTR
11	619	31.4	342	1	FUT7_HUMAN
12	579	29.4	389	1	FUT7_MOUSE
13	353	17.9	503	1	FUT7_DROME
14	295.5	15.0	425	1	FUT6_DROME
15	254.5	12.9	443	1	FUT8_DROME
16	224.5	11.4	401	1	FUT3_ARATH
17	203.5	10.3	513	1	FUT2_ARATH
18	201	10.2	501	1	FUT1_ARATH
19	106	5.4	663	1	GRIA_BACCE
20	105	5.3	537	1	UGT5_CAEEL
21	99	5.0	810	1	233A_HUMAN
22	98.5	5.0	623	1	RPOC_GUITH
23	98.5	5.0	781	1	HELI_HSVSA
24	97.5	4.9	638	1	Y153_HUMAN
25	96	4.9	387	1	CERY_CLOSR
26	96	4.9	566	1	GUNB_PAELA
27	96	4.9	2059	1	TEGU_HSV7J
28	95	4.8	1480	1	CFTR_HUMAN
29	93.5	4.7	1147	1	NRDC_HUMAN
30	92	4.7	1092	1	DHCE2_YEAST
31	91.5	4.6	1173	1	NIFU_ENTAG
32	91	4.6	482	1	YQ53_BACAN
33	91	4.6	772	1	LP1G_DROME

34	91	4.6	1026	1	EX5B_CHLUMU	Q9plt8 chlamydia m
35	90.5	4.6	584	1	MUTL_BUCAI	P57633 buchnera ap
36	90.5	4.6	986	1	EP1B_STAEP	P30195 staphylococ
37	90	4.6	438	1	RGSB_MOUSE	Q9z2h1 mus musculu
38	90	4.6	471	1	CD36_BOVIN	P26201 bos taurus
39	89.5	4.5	461	1	MYH_SCHPO	Q10159 schizosacch
40	89.5	4.5	516	1	DHCR_HUMAN	Q15392 homo sapien
41	89.5	4.5	602	1	PRIN_MYCPU	Q98d3 mycoplasma
42	89.5	4.5	934	1	SYLI_SULSO	P58176 sulfolobus
43	89	4.5	678	1	GS11_YEAST	P32477 saccharomyc
44	89	4.5	1364	1	BLM_XENLA	Q9dev9 xenopus lae
45	89	4.5	1581	1	AROL_PNECA	Q12659 p pentafunc

ALIGNMENTS

RESULT 1

FUT4_MOUSE
ID FUT4_MOUSE STANDARD: PRT: 433 AA.

AC Q11127;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Alpha-(1,3)-fucosyltransferase (EC 2.4.1.-) (Galactoside 3-L-fucosyltransferase) (Fucosyltransferase 4) (FUCT-IV).
GN FUT4 OR ELFT.

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96027607; PubMed=7559635;
RA Gersten K.M., Natsuka S., Trinchera M., Petryniak B., Kelly R.J., Hiraiwa N., Jenkins N.A., Gilbert D.J., Copeland N.G., Lowe J.B.;
RT "Molecular cloning, expression, chromosomal assignment, and tissue-specific expression of a murine alpha-(1,3)-fucosyltransferase locus corresponding to the human ELAM-1 ligand fucosyl transferase.";
RL J. Biol. Chem. 270:25047-25056(1995).

[2]
SEQUENCE FROM N.A. (SHORT FORM).
STRAIN=129/SV; TISSUE=Liver;
MEDLINE=97037075; PubMed=8862722;
Ozawa M., Muramatsu T.;
RT "Molecular cloning and expression of a mouse alpha-1,3 fucosyltransferase gene that shows homology with the human alpha-1,3 fucosyltransferase IV gene.";
RL J. Biochem. 119:302-308(1996).
CC -|- FUNCTION: MAY CATALYSE ALPHA-1,3 GLYCOSIDIC LINKAGES INVOLVED IN THE EXPRESSION OF LEWIS X/SSEA-1 AND VIM-2 ANTIGENS.
CC -|- PATHWAY: GLYCOSYLATION.
CC -|- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI.
CC -|- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -|- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN STOMACH AND COLON. IT ALSO EXPRESSED IN THE LUNG, TESTIS, UTERUS, SMALL INTESTINE AND TO A LESSER EXTENT IN SPLEEN, AND OVARY. PRESENT IN TRACE AMOUNTS IN BRAIN, THYMUS, HEART, SMOOTH MUSCLE, KIDNEY AND BONE MARROW. NOT FOUND IN LIVER, SALIVARY GLAND AND PANCREAS.
CC -|- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 10.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
DR EMBL: U33457; AAC52269.1; -;
DR EMBL: D63380; BAA09697.1; -;

DE fucosyltransferase).

GN FUT4 OR ELFT. (Human).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Periphereal blood leukocytes;

RX MEDLINE=91373370; PubMed=1716630;

RA Lowe J.B., Kukowska-Latallo J.F., Nair R.P., Larsen R.D., Marks R.M.,

RA Macher B.A., Kelly R.J., Ernst L.K.;

RT "Molecular cloning of a human fucosyltransferase gene that determines

RT expression of the Lewis x and YIM-2 epitopes but not ELAM-1-dependent

RT cell adhesion.";

RL J. Biol. Chem. 266:17467-17477(1991).

RN [2]

RN SEQUENCE FROM N.A.

RP MEDLINE=91084863; PubMed=1702034;

RA Goelz S.E., Hession C., Goff D., Griffiths B., Tizard R., Newman B.,

RA Chi-Rosso G., Lobb R.;

RT "ELFT: a gene that directs the expression of an ELAM-1 ligand.";

RL Cell 63:1349-1356(1990).

RN [3]

RN SEQUENCE OF 1-400 FROM N.A.

RX MEDLINE=92042084; PubMed=1718983;

RA Kumar R., Potvin B., Muller W.A., Stanley P.;

RT "Cloning of a human alpha(1,3)-fucosyltransferase gene that encodes

RT ELFT but does not confer ELAM-1 recognition on Chinese hamster ovary

RT cell transfectants.";

RL J. Biol. Chem. 266:21777-21783(1991).

CC -|- FUNCTION: MAY CATALYZE ALPHA-1,3 GLYCOSIDIC LINKAGES INVOLVED IN

CC -|- PATHWAY: GLYCOSYLATION.

CC -|- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND

CC FORM IN TRANS CISTERNAE OF GOLGI.

CC -|- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 10.

CC -----

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CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; M65030; AAA92977.1; -

DR EMBL; M58596; AAA63172.1; -

DR EMBL; M58597; AAA63173.1; ALT_INIT.

DR EMBL; S65161; AAB20349.1; -

DR PIR; A36340; A36340.

DR MIM; 104230; -

DR InterPro: IPR001503; Glyco_transf_10.

DR Pfam: PF00852; Glyco_transf_10; 1.

KW Transferase; Glycosyltransferase; Transmembrane; Glycoprotein;

KW Signal-anchor; Golgi stack.

FT DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 23 47 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)

FT (POTENTIAL).

FT DOMAIN 48 405 LUMENAL, CATALYTIC (POTENTIAL).

FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 190 190 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CONFLICT 87 87 P -> R (IN REF. 2 AND 3).

FT CONFLICT 241 241 E -> D (IN REF. 3).

SQ SEQUENCE 405 AA; 45569 MW; DE72E1FDC390268D CRC64;

Query Match 34.9%; Score 687.5; DB 1; Length 405;

Best Local Similarity 38.5%; Pred. No. 2.5e-44;

Matches 153; Conservative 59; Mismatches 110; Indels 75; Gaps 14;

QY 15 VCIILGCFMAC--LLIYI----RPTNSWIFSPMESASSVLKMKNFSTKTDYFNETTILV 68

DB 28 VCVLAAAGLICTALITYACGQQLPLPWA-SPTPS-----RPVGVLL 68

QY 69 WVPFGQTFDL-----TSCQAMFNIOGCHLTDRSLYKNSHAVLIHHRDI-----SW----- 115

DB 69 WPEFGGRDSAPRPDPDCPLRFNISGRCRLTDRASYGEAQAVLFHHRDLVKGPPDPWPPPW 128

QY 116 -----DLTNLPQO-----ARPPFOKWIMNLESPTHTP-OKSGIEHL 151

DB 129 GIOAHTAEVDRLVDYEEAAAAAALATSSPRPGORVWMNMFSPSHSGPLKSLASNL 189

QY 152 FNLTLTYRDSIQVPYGFGLTVSTNPFVFPVS-----KEKLVQWVYNNWNPHEHARV 203

DB 189 FNNLTSLYRSDSDVFPVGYLYPRSHP--GDPPSGLAPLSRKQGLVAVVYSHWDERQARV 246

QY 204 KYNELSKSTEIHTYQOAF--GEVYNDKNLPTISACKFYLSFSPNSIHKDIYITEKLY-NAF 261

DB 247 RYTHQLSQHVTVDFVGRGGPQVPETGLLHTVARYKFLAFENSQHLDTITEKLWRNAL 306

QY 262 LAGSPVVLGLSPRENYENIPADSFHVEDYNPSSELAKEYKVDKNKLYLSVFNWRKD 321

DB 307 LAGAVPVVLGPDNRANYERFVRGAFIHVDFFPSSASSLASYLFLDRNAPAVIRRYFHHWRS 366

QY 322 FTVNLPFWESHACLACDHVKRHQY--KSYGNLEKWF 357

DB 367 YAVHITSEWDEPWCRCVQAVORAGDRPKSIRNLASWF 403

RESULT 4

FUT3_HUMAN

ID FUT3_HUMAN STANDARD; PRT; 361 AA.

AC P21217; Q99448; Q99449;

DT 01-MAY-1991 (Rel. 18, Created)

DT 01-MAY-1991 (Rel. 18, Last sequence update)

DE 01-MAR-2002 (Rel. 41, Last annotation update)

DE Galactoside 3(4)-L-fucosyltransferase (EC 2.4.1.65) (Blood group Lewis

DE alpha-4-fucosyltransferase) (Lewis Ft) (Fucosyltransferase 3) (FUCT-

DE III)

GN FUT3 OR LE OR FT3B.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=91032981; PubMed=1977660;

RA Kukowska-Latallo J.F., Larsen R.D., Nair R.P., Lowe J.B.;

RT "A cloned human cDNA determines expression of a mouse stage-specific

RT embryonic antigen and the Lewis blood group

RT alpha(1,3/1,4)fucosyltransferase.";

RL Genes Dev. 4:1288-1303(1990).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=95378269; PubMed=7650030;

RA Cameron H.S., Szczepaniak D., Weston W.;

RT "Expression of human chromosome 19p alpha(1,3)-fucosyltransferase

RT genes in normal tissues. Alternative splicing, polyadenylation, and

RT isoforms.";

RL J. Biol. Chem. 270:20112-20122(1995).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Squamous cell carcinoma;

RA Rahim I., Schmidt L.R., Wahl D., Drayson E., Maslanik W.,

RA Stranahan P.L., Pettijohn D.E.;

RT "Isolation and expression of human alpha (1,3/1,4)

RT fucosyltransferase.";

RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.

RN [4]

RP VARIANT LE(-) MET-105.

RX MEDLINE=94059067; PubMed=8240322;

RA Elmgren A., Rydberg L., Larson G.;

RT "Genotypic heterogeneity among Lewis negative individuals.";

RL Biochem. Biophys. Res. Commun. 196:515-520(1993).

RN [5]

RP VARIANTS LE(-) ARG-20; SER-170 AND ALA-336.
RX MEDLINE-94059082; PubMed-8240337;
RA Nishihara S., Yazawa S., Iwasaki H., Nakazato M., Kudo T., Ando T.,
RA Nishimatsu H.;
RT "Alpha (1,3/1,4)fucosyltransferase (FucT-III) gene is inactivated by
RT a single amino acid substitution in Lewis histo-blood type negative
RT individuals.";
RL Biochem. Biophys. Res. Commun. 196:624-631(1993).
RN [6]
RP VARIANTS LE(-) ARG-20 AND SER-170.
RX MEDLINE-94033579; PubMed-8219240;
RA Koda Y., Kimura H., Mekada E.;
RT "Analysis of Lewis fucosyltransferase genes from the human gastric
RT mucosa of Lewis-positive and -negative individuals.";
RL Blood 82:2915-2919(1993).
RN [7]
RP VARIANTS LE(-) ARG-20 AND LYS-356.
RX MEDLINE-94342259; PubMed-8063716;
RA Mollicone R., Requinne I., Kelly R.J., Fletcher A., Watt J., Oriol R.;
RA Chatfield S., Aziz A., Cameron H.S., Weston B.W., Lowe J.B.;
RT "Molecular basis for Lewis alpha(1,3/1,4)-fucosyltransferase gene
RT deficiency (FUT3) found in Lewis-negative Indonesian pedigrees.";
RL J. Biol. Chem. 269:20987-20994(1994).
RN [8]
RP VARIANT LE(-) LYS-356.
RX MEDLINE-95050753; PubMed-7961897;
RA Nishihara S., Narimatsu H., Iwasaki H., Yazawa S., Akamatsu S.,
RA Ando T., Seno T., Narimatsu I.;
RT "Molecular genetic analysis of the human Lewis histo-blood group
RT system.";
RL J. Biol. Chem. 269:29271-29278(1994).
RN [9]
RP VARIANTS LE(-) ARG-68; MET-105 AND LYS-356.
RX MEDLINE-96243526; PubMed-8801770;
RA Elmgren A., Boerjeson C., Svensson L., Rydberg L., Larson G.;
RT "DNA sequencing and screening for point mutations in the human Lewis
RT 'FUT3' gene enables molecular genotyping of the human Lewis blood
RT group system.";
RL Vox Sang. 70:97-103(1996).
RN [10]
RP VARIANTS LE(-) ARG-68 AND MET-105.
RX MEDLINE-97413801; PubMed-9268337;
RA Elmgren A., Mollicone R., Costache M., Boerjeson C., Oriol R.,
RA Harrington J., Larson G.;
RT "Significance of individual point mutations, T202C and C314T, in the
RT human Lewis 'FUT3' gene for expression of Lewis antigens by the human
RT alpha1,3/1,4'-fucosyltransferase, fuc-TIII.";
RL J. Biol. Chem. 272:21994-21998(1997).
RN [11]
RP VARIANTS LE(+) K-102 AND A-124, AND VARIANTS LE(-) N-162; R-223 AND
RP M-270.
RX MEDLINE-98366989; PubMed-9703429;
RA Pang H., Liu Y., Koda Y., Soejima M., Jia J., Schlaphoff T.,
RA du Toit E.D., Kimura H.;
RT "Five novel missense mutations of the Lewis gene 'FUT3' in African
RT 'Xhosa' and Caucasian populations in South Africa.";
RL Hum. Genet. 102:675-680(1998).
CC -1- FUNCTION: MAY CATALYZE ALPHA-1,3 AND ALPHA-1,4 GLYCOSIDIC LINKAGES
CC INVOLVED IN THE EXPRESSION OF VIM-2, LEWIS A, LEWIS B, SIALYL
CC LEWIS X AND LEWIS X/SSA-1 ANTIGENS. MAY BE INVOLVED IN BLOOD
CC GROUP LEWIS DETERMINATION; LEWIS-POSITIVE (LE(+)) INDIVIDUALS
CC HAVE AN ACTIVE ENZYME WHILE LEWIS-NEGATIVE (LE(-)) INDIVIDUALS
CC HAVE AN INACTIVE ENZYME.
CC -1- CATALYTIC ACTIVITY: GDP-L-FUCOSE + 1,3-BETA-D-GALACTOSYL-
CC N-ACETYL-D-GLUCOSAMINYL-R = GDP + 1,3-BETA-D-GALACTOSYL-
CC (ALPHA-1,4-L-FUCOSYL)-N-ACETYL-D-GLUCOSAMINYL-R.
CC -1- PATHWAY: GLYCOSYLATION.
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC FORM IN TRANS CISTERNAE OF GOLGI.
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN STOMACH, COLON, SMALL
CC INTESTINE, LUNG AND KIDNEY AND TO A LESSER EXTENT IN SALIVARY
CC GLAND, BLADDER, UTERUS AND LIVER.
CC -1- MISCELLANEOUS: ALSO ACTS ON THE CORRESPONDING 1,4-GALACTOSYL

CC DERIVATIVE, FORMING 1,3-L-FUCOSYL LINKS.
CC -1- SIMILARITY: BELONGS TO THE FUCOSYLTRANSFERASE FAMILY 10.
CC -----
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CC -----
CC EMBL: X53578; CAA37641.1; -
DR EMBL: U27328; AAC50187.1; -
DR EMBL: U27326; AAC50185.1; -
DR EMBL: U27327; AAC50186.1; -
DR EMBL: D89324; BAA13941.1; -
DR EMBL: D89325; BAA13942.1; -
DR EMBL: AF131913; AAD33314.1; -
DR PIR: A36669; A36669.
DR MIM: 111100; -
DR InterPro; IPR001503; Glyco_transf_10.
KW Transferease; Glycosyltransferase; Glycoprotein; Transmembrane;
KW Pfam; PF00852; Glyco_transf_10; 1.
FT Signal-anchor; Golgi stack; Polymorphism; Blood group antigen.
FT DOMAIN 1 15
FT TRANSMEM 16 34
FT DOMAIN 35 361
FT CARBOHYD 154 154
FT CARBOHYD 185 185
FT VARIANT 20 20
FT VARIANT 68 68
FT VARIANT 102 102
FT VARIANT 105 105
FT VARIANT 124 124
FT VARIANT 162 162
FT VARIANT 170 170
FT VARIANT 223 223
FT VARIANT 270 270
FT VARIANT 336 336
FT VARIANT 356 356
FT SEQUENCE 361 AA; 42117 MW; BF439804F19C284 CRC64;
FT Query Match 33.9%; Score 667; DB 1; Length 361;
FT Best Local Similarity 43.1%; Pred. No. 7.4e-43;
FT Matches 131; Conservative 55; Mismatches 98; Indels 20; Gaps 9;
QY 66 ILVWVWPFGQTDFDLTSCQAMF-NIQGHLTLTDRSLYKNSHAVLIHRDISWDL-----TN 119
Db 65 ILLWTFPHIPVALSRCSEVPGVADCHITADRVKVPQADTVIVHH---WDINSNPKSR 120
QY 120 LPOQARPPFOKWIWMNLESPTHTPKSGIEHLENLTLYRSDSDIQVPYGLTV-STNPF 178
Db 121 LPPSPRQGGQWIWFWNLEPPNCOHLEADRYFNLTYSRSDSDIFTPTGWLPEWSCQA 180
QY 179 --VPEVSKELVCWVYVSNPNPEHARVYKYNELSKSTEIHTYQAFGEYVNDKNLIPTIS 236
Db 181 HPLNLAKTELAVAWVSNMKNPQSRVRYQSQAHLKVDVYKSH-KPLPKGTMMETLS 239
QY 237 ACKPYLSEFNSIHKDYITEKLY-NAFLAGSVVYVGLGSPRENENYIPADSFHVEDYNSP 295
Db 240 RYKPYLAFENSLHPDYITEKLRNLEAWVVPVYVGLGSPRSNRYERFLPDPAFIHYDDQSP 299

QY 296 SELAKYLKEVDKNNKLYLSYFNHRKDFVNLPR--FWESHACIACDHWKHOEYKSVGNL 353
 Db 300 KDLARYLQELDKHARYLSYFWRRETLR---PRFSWALDFCKACKWKLQESRYQTVRSI 356
 QY 354 EKWF 357
 Db 357 AAWF 360

RESULT 5
 FUT5_HUMAN STANDARD; PRT; 374 AA.
 AC Q11128;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Alpha-(1,3)-fucosyltransferase (EC 2.4.1.65) (Galactoside 3-L-fucosyltransferase) (Fucosyltransferase 5) (FUCT-V).
 GN FUT5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Periphereal blood leukocytes;
 RX MEDLINE=952156161; PubMed=1740457;
 RA Weston B.W., Nair R.P., Larsen R.D., Lowe J.B.;
 RT "Isolation of a novel human alpha (1,3)fucosyltransferase gene and molecular comparison to the human Lewis blood group alpha (1,3/1,4)fucosyltransferase gene. Synthetic, homologous, nonallelic genes encoding enzymes with distinct acceptor substrate specificities.";
 RT J. Biol. Chem. 267:4152-4160(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon, Kidney, and Liver;
 RX MEDLINE=95378269; PubMed=7650030;
 RA Cameron H.S., Szczepaniak D., Weston B.W.;
 RT "Expression of human chromosome 19p alpha(1,3)-fucosyltransferase genes in normal tissues. Alternative splicing, polyadenylation, and isoforms.";
 RT J. Biol. Chem. 270:20112-20122(1995).
 RL CC -1- FUNCTION: MAY CATALYZE ALPHA-1,3 GLYCOSIDIC LINKAGES INVOLVED IN THE EXPRESSION OF VIM-2, LEWIS X/SSEA-1 AND SIALYL LEWIS X ANTIGENS.
 CC -1- CATALYTIC ACTIVITY: GDP-L-FUCOSE + 1,3-BETA-D-GALACTOSYL-N-ACETYL-D-GLUCOSAMINYL-R = GDP + 1,3-BETA-D-GALACTOSYL-(ALPHA-1,4-L-FUCOSYL)-N-ACETYL-D-GLUCOSAMINYL-R.
 CC -1- PATHWAY: GLYCOSYLATION.
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI.
 CC -1- TISSUE SPECIFICITY: LIVER, COLON AND TESTIS AND TRACE AMOUNTS IN T-CELLS AND BRAIN.
 CC -1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 10.
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 CC -----
 DR EMBL; M81485; AAA98117.1; -;
 DR EMBL; U27329; AAC50188.1; -;
 DR EMBL; U27330; AAC50189.1; -;
 DR MIM; 136835; -;
 DR InterPro; IPR001503; Glyco_transf_10.
 DR Pfam; PF00852; Glyco_transf_10; 1.
 KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal-anchor; Golgi stack.

FT DOMAIN 1 15 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 16 34 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
 FT LUMENAL, CATALYTIC (POTENTIAL).
 FT CARBOHYD 35 374 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 60 60 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 167 167 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 374 AA; 43008 MW; B825281521B57939 CRC64;

Query Match 33.9%; Score 667; DB 1; Length 374;
 Best Local Similarity 43.7%; Pred. No. 7.7e-43;

Matches 131; Conservative 58; Mismatches 99; Indels 12; Gaps 8;

QY 66 ILVVMVPFGQTDLTSCQAMF-NIQGCHLTDRSLYNKSHAVLIHHRDISMD-LTNLPQQ 123
 Db 78 ILLWTVPFNTPVALPRCSEMPVGAACDNITADSSVYQADAVIVHHWDIMYNSANLPPP 137
 QY 124 ARPPFQKWIWNLESPTHTPKSGIEHLENLTLTYRSDIOVPYGFGLTV-STNPF--VF 180
 Db 138 TRPGQGRWIWFSESPSNCRHLEALDGYFNLTWISYSDSDIFTYPGWLEPWSGQPAHPPL 197
 QY 181 EVPSKEKLVCMVYNNWNPENHARVYKYNELSKSIEHTHYGOAFGEYVNDKLLIPTISACKF 240
 Db 198 NLSAKTELVAVAYSNWKPDSARVYQSLQAHKLVYVYGRSH-KPLPKGTMTETLSRYKF 256
 QY 241 YLSFENSIHKDYITEKLY-NAFLAGSVVYVLPSPRENYENIIPADSFHVEDYNSPSELA 299
 Db 257 YLAFENSLHPDYITEKLRNLEAWAVPVVLPSPRSYERFLPPDPADFIHVDDEQSPKDLA 316
 QY 300 KYLKEVDKNNKLYLSYFNHRKDFVNLPR--FWESHACIACDHWKHOEYKSVGNLEKWF 357
 Db 317 RYLQELDKHARYLSYFWRRETLR---PRFSWALDFCKACKWKLQESRYQTVRSI 373

RESULT 6

FUT5_PANTR STANDARD; PRT; 374 AA.
 AC P56433;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Alpha-(1,3)-fucosyltransferase (EC 2.4.1.65) (Galactoside 3-L-fucosyltransferase) (fucosyltransferase 5) (FUCT-V).
 GN FUT5.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98037800; PubMed=9368041;
 RA Costache M., Apoil P.-A., Cailliau A., Elmgren A., Larson G., Henry S., Blancher A., Iordachescu D., Oriol R., Mollicone R.;
 RT "Evolution of fucosyltransferase genes in vertebrates.";
 RL J. Biol. Chem. 272:29721-29728(1997).
 RL CC -1- FUNCTION: MAY CATALYZE ALPHA-1,3 GLYCOSIDIC LINKAGES INVOLVED IN THE EXPRESSION OF VIM-2, LEWIS X/SSEA-1 AND SIALYL LEWIS X ANTIGENS (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: GDP-L-FUCOSE + 1,3-BETA-D-GALACTOSYL-N-ACETYL-D-GLUCOSAMINYL-R = GDP + 1,3-BETA-D-GALACTOSYL-(ALPHA-1,4-L-FUCOSYL)-N-ACETYL-D-GLUCOSAMINYL-R.
 CC -1- PATHWAY: GLYCOSYLATION.
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI.
 CC -1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 10.
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 CC -----
 DR EMBL; M81485; AAA98117.1; -;
 DR EMBL; U27329; AAC50188.1; -;
 DR EMBL; U27330; AAC50189.1; -;
 DR MIM; 136835; -;
 DR InterPro; IPR001503; Glyco_transf_10.
 DR Pfam; PF00852; Glyco_transf_10; 1.
 KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal-anchor; Golgi stack.

```

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CC -----
DR EMBL: Y14034; CAA74361.1; - Glyco.transf_10.
DR InterPro: IPR001503; Glyco.transf_10.
DR Pfam: PF00852; Glycosyltransferase; Glycoprotein; Transmembrane;
KW Signal-anchor; Golgi stack.
KW DOMAIN 1 15 CYTOPLASMIC (POTENTIAL).
KW TRANSMEM 16 34 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT FT DOMAIN 35 374 LUMENAL, CATALYTIC (POTENTIAL).
FT FT CARBOHYD 60 60 N-LINKED (GLCNAC. .) (POTENTIAL).
FT FT CARBOHYD 105 105 N-LINKED (GLCNAC. .) (POTENTIAL).
FT FT CARBOHYD 167 167 N-LINKED (GLCNAC. .) (POTENTIAL).
FT FT CARBOHYD 198 198 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 374 AA; 43034 MW; 3F35DE8A8F1A2E2 CRC64;

Query Match 33.8%; Score 666; DB 1; Length 374;
Best Local Similarity 43.0%; Pred. No. 9,2e-43;
Matches 129; Conservative 59; Mismatches 100; Indels 12; Gaps 7;

QY 66 ILVWVWPGTDLTSCQAMF-NIOGCHLTDRSLYNKSHAVLIHHRDISWD-LTNLPQQ 123
DB 78 ILLWTWPFNPVALPCSEKVPKADCNITADSNVYQADAVIVHWDIMNPSANLPP 137
QY 124 ARPPKQKWTMNLSPHTHTPOKSGIEHLENLTLYRRSDIOVPYGLTVSTNPV---F 180
DB 138 TRPGQGRWLWFSNESPSCNHRLEADGFLNLTMSRSDSDIFTPTGWLQPSGQVHPPL 197
QY 181 EYPSKEKLVCVVSNWNNPEHARVYKYNELSKSIEHTYQOAPGEYVNDKNLIPTISACKF 240
DB 198 NLSATELVAVSNWNGNSARVYQSLQHLKVDVYGRSH-KPLPGTMMETLSRYKF 256
QY 241 YLSFNSIHKDYITEKLY-NAFLAGSPVVLGSPRSYENYIPADSFHVEDYNSPSELA 299
DB 257 YLAFNSLHPDYITEKLRNLEAWAVPVVLGSPRSNTERELPPDAFTHVDVDFQSPKDLA 316
QY 300 KYLKEVDKNNKLYLSYFNWRKDFTVNLPR--FWESHACLDHVRHQRQYKSVGNLEKWF 357
DB 317 RYLQELDKDHARYLSYFRWRETLR---PRSFNSWALDFCKACKWLOQRYQTVRSIAAWF 373

RESULT 7
ID FUT3_BOVIN STANDARD; PRT; 365 AA.
AC Q11126;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Galactoside 3(4)-L-fucosyltransferase (EC 2.4.1.65) (Blood group Lewis
DE alpha-4-fucosyltransferase) (Lewis Fx) (Fucosyltransferase 3) (FUCT-
DE ILL) (FUTB).
GN FUT3.
OS Bos taurus (Bovine).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
CC Bovidae; Bovinae; Bos.
CC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-97236840; PubMed=9079712;
RA Oulmouden A., Wierinckx A., Petit J.-M., Costache M., Palcic M.M.,
RA Mollicone R., Oriol R., Julien R.;
RT "Molecular cloning and expression of a bovine alpha(1,3)-
RT fucosyltransferase gene homologous to a putative ancestor gene of the
RT human FUT3-FUT5-FUT6 cluster."
RL J. Biol. Chem. 272:8764-8773(1997).
CC -!- FUNCTION: MAY CATALYSE ALPHA-1,3 AND ALPHA-1,4 GLYCOSIDIC LINKAGES
CC INVOLVED IN THE EXPRESSION OF SIALYL LEWIS X AND LEWIS X/SEA-1
CC ANTIGENS. IT MAY BE INVOLVED IN BLOOD GROUP LEWIS DETERMINATION.
CC -!- CATALYTIC ACTIVITY: GDP-L-FUCOSE + 1,3-BETA-D-GALACTOSYL-
CC N-ACETYL-D-GLUCOSAMINYL-R = GDP + 1,3-BETA-D-GALACTOSYL-
CC (ALPHA-1,4-L-FUCOSYL)-N-ACETYL-D-GLUCOSAMINYL-R.
GN

-!- PATHWAY: GLYCOSYLATION.
-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
-!- FORM IN TRANS CISTERNAE OF GOLGI.
-!- TISSUE SPECIFICITY: LIVER, KIDNEY, LUNG AND BRAIN.
-!- MISCELLANEOUS: ALSO ACTS ON THE CORRESPONDING 1,4-GALACTOSYL
DERIVATIVE, FORMING 1,3-L-FUCOSYL LINKS.
-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 10.

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EMBL: X87810; CAA61079.1; -
InterPro: IPR001503; Glyco.transf_10.
Pfam: PF00852; Glycosyltransferase; Glycoprotein; Transmembrane;
KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
KW Signal-anchor; Golgi stack.
KW DOMAIN 1 14 CYTOPLASMIC (POTENTIAL).
KW TRANSMEM 15 34 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT FT DOMAIN 35 365 LUMENAL, CATALYTIC (POTENTIAL).
FT FT CARBOHYD 100 100 N-LINKED (GLCNAC. .) (PROBABLE).
FT FT CARBOHYD 158 158 N-LINKED (GLCNAC. .) (PROBABLE).
FT FT CARBOHYD 189 189 N-LINKED (GLCNAC. .) (PROBABLE).
SQ SEQUENCE 365 AA; 42654 MW; 18715A361B0025D3 CRC64;

Query Match 33.8%; Score 665; DB 1; Length 365;
Best Local Similarity 38.9%; Pred. No. 1.1e-42;
Matches 143; Conservative 68; Mismatches 115; Indels 42; Gaps 12;

QY 11 PFLIVCIILG-CFMACLLI---YIKPTNSWI-----FSPMESASSVLKMKNFSTKTDY 60
DB 18 PGLLLQLLLALCFSTYLRMSQEKPKPKPMWSELGAPSOATEGSSAHLPLR----- 68
QY 61 FNETTILVWVWPGTDLTSCQAMF-NIOGCHLTDRSLYNKSHAVLIHHRDISW-DLT 118
DB 69 -----VLLWTWPFNPVALPCSEKSELPGTADQCLTVNSESYPQADAVLVHREYSHRQPM 123
QY 119 NLQOARPPFOKWTMNLSPHTHTPOKSGIEHLENLTLYRRSDIOVPYGLF-----T 172
DB 124 QLPPSPRPFGQGRWVWFSNESPSCNHRLEADGFLNLTMSRSDSDIFTPTGWLQPSGQV 183
QY 173 VSTNPFVEVPSKEKLVCVVSNWNNPEHARVYKYNELSKSIEHTYQOAPGEYVNDKNLI 232
DB 184 VET---LLNISAKTLKLVAVVSNWNNPTDSIRVQYKLLKPLHLOVDVYGR-FHTPLPALMA 239
QY 233 PTISACKPYLSFNSIHKDYITEKLY-NAFLAGSPVVLGSPRSYENYIPADSFHVED 291
DB 240 KOLSOYKFLAFENSLHPDYITEKLRNLEAWAVPVVLGSPRSYENYIPADSFHVED 299
QY 292 YNSPSELAKLYKEVDKNNKLYLSYFNWRKDFTVNLPR--FWESHACLDHVRHQRQYK 349
DB 300 FQSPKDLAQYLLALDKDYASYLNYFRWRETLR---PRSFNSWALDFCKACKWLOQRYQTV 356
QY 350 VGNLEKWF 357
DB 357 VPSIASWF 364

RESULT 8
ID FUT6_HUMAN STANDARD; PRT; 359 AA.
AC P51993;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Alpha-(1,3)-fucosyltransferase (EC 2.4.1.65) Galactoside 3-L-
DE fucosyltransferase) (Fucosyltransferase 6) (FUCT-VI).
DE FUT6 OR FCT3A.
GN

```


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EMBL; Y14033; CAA74360.1; -
 InterPro: IPR001503; Glyco_transf_10.
 Pfam: PF00852; Glyco_transf_10; 1.
 Transferrase; Glycosyltransferase; Glycoprotein; Transmembrane;
 Signal-anchor; Golgi stack; Polymorphism.
 DOMAIN 1 14
 TRANSMEM 15 34
 (POTENTIAL).
 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 (POTENTIAL).
 LUMENAL, CATALYTIC (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 R -> G (IN ALLELE B).
 V -> M (IN ALLELE B).
 SEQUENCE 372 AA; 43233 MW; 649CFB8CA7BD74C CRC64;

Query Match 33.5%; Score 660; DB 1; Length 372;
 Best Local Similarity 43.3%; Pred. No. 2.6e-42;
 Matches 130; Conservative 57; Mismatches 101; Indels 12; Gaps 8;
 QY 66 ILVWVWPGQTDLSCQAMF-NIOGCHLTDRSLYNKSHAVLIHHRDISWD-LTNLPQQ 123
 DB 76 ILLWTWPFHPVALSRCEMPEGAADCHTADRKVYPOADAVIVHHWIMYNPKSRLLPS 135
 QY 124 ARPPFQKWMNLESTPTTPQKSGIEHLNLTLYRRSDIQVPGFTLV-STNPF--VF 180
 DB 136 PRPQSGRWTFNLEPPNCOHLEADRYFNLTMSYRSDDIFTYPYGLWLEPWSGQAPHPPL 195
 QY 181 EYPSKEKLVCVVSNWNNPEHARVYKYNELSKSIEHTYQGAFFGVNDKNLPTISACKF 240
 DB 196 NLSAKTELVAWAVSNWKLDSARVYVYQSLQAILKLVVDVYGRSH-KPLPKGTMTLSRYKF 254
 QY 241 YLSFENSIIHKDYITEKLY-NAFLAGSVVPVLPSPRENENYIPADSFTHVEDYNSPSELA 299
 DB 255 YLAFENSLHPDYITEKLWRNALEAWVPVVLGSPRSNRYERFLPDFAIHVDVDFQSPKDLA 314
 QY 300 KYLKEVDKNNKLYLYFENWRKDFTVNLRP--FWESHACLDHVKRQKYSVGNLEKWF 357
 DB 315 RYLQELDKDHARYLSYFRWRETLR---PRSFWDALDFCKACWKLOQESRYQTMRSIAAWF 371

RESULT 10
 ID FUT6 PANTR STANDARD; PRT; 359 AA.
 AC P56434;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DE 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Alpha-(1,3)-fucosyltransferase (EC 2.4.1.65) (Galactoside 3-L-fucosyltransferase) (Fucosyltransferase 6) (FUCT-VI).
 GN FUT6.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98037800; PubMed=9368041;
 RA Costache M., Apoll P.-A., Caillaue A., Elmgren A., Larson G., Henry S., Blancher A., Iordachescu D., Oriol R., Mollicone R.;
 RT "Evolution of fucosyltransferase genes in vertebrates.";
 RL J. Biol. Chem. 272:29721-29728(1997).
 CC -1- FUNCTION: ENZYME INVOLVED IN THE BIOSYNTHESIS OF THE E-SELECTIN LIGAND, SIALYL-LEWIS X, CATALYZES THE TRANSFER OF FUCOSE FROM GDP-BETA-FUCOSE TO ALPHA-2,3 SIALYLATED SUBSTRATES (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: GDP-L-FUCOSE + 1,3-BETA-D-GALACTOSYL-N-ACETYL-D-GLUCOSAMINYL-R = GDP + 1,3-BETA-D-GALACTOSYL-(ALPHA-1,4-L-FUCOSYL)-N-ACETYL-D-GLUCOSAMINYL-R.
 CC

-1- PATHWAY: GLYCOSYLATION.
 -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI (BY SIMILARITY).
 -1- POLYMORPHISM: THERE ARE TWO ALLELES, A AND B. ALLELE A HAS PRO-124, GLN-172 AND VAL-192. ALLELE B HAS LEU-124, GLU-172 AND ALA-192.
 -1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 10.

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EMBL; Y14033; CAA74362.1; -
 InterPro: IPR001503; Glyco_transf_10.
 Pfam: PF00852; Glyco_transf_10; 1.
 Transferrase; Glycosyltransferase; Glycoprotein; Transmembrane;
 Signal-anchor; Golgi stack; Polymorphism.
 DOMAIN 1 14
 TRANSMEM 15 34
 (POTENTIAL).
 SIGNAL-ANCHOR (POTENTIAL).
 LUMENAL, CATALYTIC (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 P -> L (IN ALLELE B).
 VARIANT 124 124
 VARIANT 172 172
 VARIANT 192 192
 V -> A (IN ALLELE B).
 SEQUENCE 359 AA; 41892 MW; 207C3DC29B2BFDD3 CRC64;

Query Match 33.5%; Score 659.5; DB 1; Length 359;
 Best Local Similarity 41.8%; Pred. No. 2.7e-42;
 Matches 130; Conservative 62; Mismatches 106; Indels 13; Gaps 8;
 QY 55 STKTDYNETILVWVWPGQTDLSCQAMF-NIOGCHLTDRSLYNKSHAVLIHHRDI 113
 DB 53 STGTPTSIPILLWTWPFHPVALSRCEMPEGAADCHTADRKVYPOADAVIVHHRE 112
 QY 114 SWD-LTNLPQARPPFQKWMNLESTHTTPQKSGIEHLNLTLYRRSDIQVPGFTLV 172
 DB 113 MYNSAQLPSPRQGRQWIFSMESPSNCHLEALDGYFNLTMSYRSDDIFTYPYGLW 172
 QY 173 VSTNPFV---FEVPSKEKLVCVVSNWNNPEHARVYKYNELSKSIEHTYQGAFFGVNDK 229
 DB 173 PWSGQPVHPPLNLSAKTELVAWAVSNWGNPSARVYVYQSLQAILKLVVDVYGRSH-KPLPQG 231
 QY 230 NLIPTISACKFYLSEFNSIIHKDYITEKLY-NAFLAGSVVPVLPSPRENENYIPADSFTH 288
 DB 232 TMTETLSRYKFLAFENSLHPDYITEKLWRNALEAWVPVVLGSPRSNRYERFLPDFAIH 291
 QY 289 VEDYNSPSELAKYKLVKNNKLYLYFENWRKDFTVNLRP--WESHACLDHVKRQK 346
 DB 292 VDDFQSPKDLARYLQELDKDHARYLSYFRWRETLR---PRFWSALAFCKACWKLOQESR 348
 QY 347 YKSVGNLEKWF 357
 DB 349 YQT-RSIAAWF 358

RESULT 11
 ID FUT7 HUMAN STANDARD; PRT; 342 AA.
 AC Q11130;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DE 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Alpha-(1,3)-fucosyltransferase (EC 2.4.1.-) (Galactoside 3-L-fucosyltransferase) (Fucosyltransferase 7) (FUCT-VII) (Selectin-ligand synthase).
 GN FUT7.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94266898; PubMed=8207002;
 RA Natsuka S., Gersten K.M., Zenita K., Kannagi R., Lowe J.B.;
 RT "Molecular cloning of a cDNA encoding a novel human leukocyte
 alpha-1,3-fucosyltransferase capable of synthesizing the sialyl
 Lewis x determinant.";
 RL J. Biol. Chem. 269:16789-16794(1994).
 RN [2]
 RP REVISIONS
 RX MEDLINE=94327669; PubMed=8051184;
 RA Natsuka S., Gersten K.M., Zenita K., Kannagi R., Lowe J.B.;
 RT "Molecular cloning of a cDNA encoding a novel human leukocyte
 alpha-1,3-fucosyltransferase capable of synthesizing the sialyl
 Lewis x determinant.";
 RL J. Biol. Chem. 269:20806-20806(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94237894; PubMed=8182079;
 RA Sasaki K., Kurata K., Funayama K., Nagata M., Watanabe E., Ohta S.,
 RA Hanai N., Nishi T.;
 RT "Expression cloning of a novel alpha 1,3-fucosyltransferase that is
 involved in biosynthesis of the sialyl Lewis x carbohydrate
 determinants in leukocytes.";
 RL J. Biol. Chem. 269:14730-14737(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Hiraawa N., Hiraawa M., Kannagi R.;
 RT "The human selectin-ligand synthase (hFuc-T VII) gene structure and
 characterization of the promoter.";
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: MAY CATALYZE ALPHA-1,3 GLYCOSIDIC LINKAGES INVOLVED IN
 THE EXPRESSION OF SIALYL LEWIS X ANTIGENS.
 CC -1- CATALYTIC ACTIVITY: GDP-L-FUCOSE + ALPHA-2,3-NEU-N-ACETYL-1,4-
 BETA-D-GALACTOSYL-N-ACETYL-D-GLUCOSAMINYL-R = GDP + ALPHA-2,3-
 NEU-N-ACETYL-1,4-BETA-D-GALACTOSYL-(ALPHA-1,3-L-FUCOSYL)-
 N-ACETYL-D-GLUCOSAMINYL-R.
 CC -1- PATHWAY: GLYCOSYLATION.
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
 FORM IN TRANS CISTERNAE OF GOLGI.
 CC -1- TISSUE SPECIFICITY: LEUKOCYtic/MYELOID LINEAGE CELLS.
 CC -1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 10.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X76031; CAA54962.1; -;
 DR EMBL; U11282; AAA20468.1; -;
 DR EMBL; U08112; AAA56869.1; -;
 DR EMBL; AB012668; BAA32819.1; -;
 DR MIM; 602030; -;
 DR InterPro: IPR001503; Glyco_transf_10;
 DR Pfam: PF00852; Glyco_transf_10; 1.
 KW Transferase; Glycosyltransferase; Transmembrane; Glycoprotein;
 KW Signal-anchor; Golgi stack.
 FT DOMAIN 1 14
 FT TRANSMEM 15 36
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT LUMENAL, CATALYTIC (POTENTIAL).
 FT N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 291 291
 FT N-LINKED (GLCNAC...) (POTENTIAL).
 FT CONFLICT 161 162
 FT GP -> A (IN REF. 1; AAA56869).
 FT CONFLICT 304 305
 FT RL -> SV (IN REF. 1; AAA56869).
 FT SEQUENCE 342 AA; 39238 MW; D31BFF9DD64DFAB CRC64;

Query Match 31.4%; Score 619; DB 1; Length 342;
 Best local Similarity 43.0%; Pred. No. 2.7e-39;
 Matches 129; Conservative 49; Mismatches 108; Indels 14; Gaps 8;
 QY 65 TILVWVPF-GOTFDLTS--COAMENIOGCHLTDRSLYNKSHAVLIHHRDISWDLNLP 121
 DB 48 TILVWHPFTDQPPPLSDTC-TRYGIARCHLSNRSLLASADAVVFHRLQTRRSLP 106
 QY 122 QOARPPQKWIWMNLESPHTPQKSGIEHLENLTITLRRSDIOVPYGFGLVSTNPFVFE 181
 DB 107 LAQRPGCPWVWASMESPSHTGLSHLGIENWLSYRDSDFVYGRLEPHGWPSP-P 165
 QY 182 VPSKEKLVCVVSNWNNPEHARVYKYNLSKSIETHYQOAFGEYVNDKNLPTISACKFY 241
 DB 166 LPAKRSVAAWVSNFQERQLRARLYRQLAPHLRVDVFGRRNGRCLASCCLVPTVAQVRFY 225
 QY 242 LSFENSHKDYITEKLY-NAFLAGSVPVVLGSPENYENYIPADSFTHVEDYNSPELAK 300
 DB 226 LSFENSHRDYITEKFNALVAGTVPVVLGPPRTATYFAFPADAFVHVDVFGSARELAA 285
 QY 301 YLKEVDKNNKLYLSYFNWRKDFTVNLPFWESHACLACD---HVKRHOEYKSVGNLEKWF 357
 DB 286 FL--TGMNESRYQREFAWRDLRVLPFDWRECAICDRPHLPQRSQVYE---DLEGWF 340
 RESULT 12
 ID FUT7_MOUSE STANDARD; PRT; 389 AA.
 AC Q1131;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Alpha-(1,3)-fucosyltransferase (EC 2.4.1.-) (Galactoside 3-L-
 DE fucosyltransferase) (Fucosyltransferase 7) (FUCT-VII).
 GN FUT7
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NTH;
 RX MEDLINE=96215226; PubMed=8626519;
 RA Smith P.L., Gersten K.M., Petryniak B., Kelly R.J., Rogers C.,
 RA Natsuka Y., Alford J.A. III, Scheidegger E.P., Natsuka S., Lowe J.B.;
 RT "Expression of the alpha(1,3)fucosyltransferase Fuc-TVII in lymphoid
 aggregate high endothelial venules correlates with expression of L-
 selectin ligands.";
 RT J. Biol. Chem. 271:8250-8259(1996).
 CC -1- FUNCTION: MAY CATALYZE ALPHA-1,3 GLYCOSIDIC LINKAGES INVOLVED IN
 THE EXPRESSION OF SIALYL LEWIS X ANTIGENS.
 CC -1- CATALYTIC ACTIVITY: GDP-L-FUCOSE + ALPHA-2,3-NEU-N-ACETYL-1,4-
 BETA-D-GALACTOSYL-N-ACETYL-D-GLUCOSAMINYL-R = GDP + ALPHA-2,3-
 NEU-N-ACETYL-1,4-BETA-D-GALACTOSYL-(ALPHA-1,3-L-FUCOSYL)-
 N-ACETYL-D-GLUCOSAMINYL-R.
 CC -1- PATHWAY: GLYCOSYLATION.
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
 FORM IN TRANS CISTERNAE OF GOLGI.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE
 PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG AND BONE MARROW AND
 TO A MUCH LESSER EXTENT IN SPLEEN, SALIVARY GLAND AND SKELETAL
 MUSCLE.
 CC -1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 10.
 CC -----
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SQL	SEQUENCE	503 AA;	59159 MW;	D9DA06078E6010C2	CRC64;
	Query Match	17.9%;	Score 353;	DB 1;	Length 503;
	Best Local Similarity	32.5%;	Pred. No. 3.3e-19;		
	Matches	96;	Conservative 42;	Mismatches 105;	Indels 52; Gaps
QY	88 IQCHLTTRSLYNKSHAVLIHIROISWDLTNLPQOARPPFOKWIM--NLSPHTTHPK 145	:	:	:	:
Db	202 VDTCELTANRDLASTAMILYKDHYIPTGT-----RRPSNSKQVSMLYLPCPYHT-QN 254	:	:	:	:
QY	146 SGTEHLFNLTLTYRRSDIQPV-----GFLTVTSTPNFFVEVPSEKELCYCW 191	:	:	:	:
Db	255 VKYPDAINWTATYRDSITVAPEYKQKYDYTKVQQEQBDINTSVN-----KTKKVAM 306	:	:	:	:
QY	192 VVSNNPNEHARVKYYNELSKSIEIHTYGQAIFYVDKNLIPITSAC-----KFYL 243	:	: :	:	: :
Db	307 FVSCNGCARNGRLQYAHLOKYLEVDIYG-ACGNFKCSRS---TADKCFLINDYKFLYA 362	:	: :	:	: :
QY	244 FENSIHKDYITEKLY-NAFLAGSVVVLPGSRRENYENYIPASOFIHVEDYNSPELAKYL 302	:	:	:	:
Db	363 FENSNCNDYITERFFVNALNRRLPLTVMGARDEYVSAPRRSYIHVDFESSPKELAELY 422	:	: :	:	: :
QY	303 KEVDKNNKLYSFENRKDOFTNLPFWESHACLADHVKKHQEKYSVGNLEKWF 357	:	: :	:	: :
Db	423 RLIDHDDELNSYFKWKGTGEFTNTYYW----CRVCATLHNEEQURK-----PRWY 469	:	: :	:	: :
RESULT 14	FUTC_DROME				
ID	FUTC_DROME	STANDARD;	PRT;	425 AA.	
AC	PF03088;				
DC	01-MAR-2002 (Rel. 41, Created)				
DT	01-MAR-2002 (Rel. 41, Last sequence update)				
DT	01-MAR-2002 (Rel. 41, Last annotation update)				
DE	Alpha-(1,3)-fucosyltransferase C (EC 2.4.1.-) (Galactoside 3-L-fucosyltransferase).				
DE	FUCIC.				
GN	Drosophila melanogaster (Fruit fly).				
OS	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;				
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;				
QC	Phlebotomidae; Drosophilidae; Drosophila.				
OX	NCBI_TaxID=7227;				
RP	[1]				
RN	SEQUENCE FROM N.A.				
RC	STRAIN=Canton-S.				
RC	MDLINE=21359431; PubMed=11382750;				
RX	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon K.C., Rogers Y.-H.C., Blazef R.G., Champagne M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D., Ballou R.M., Basu A., Bakendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berhan B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J.J., Brokstein P., Brotter P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlike C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelian A.C., Ferraz C., Ferreira S., Fleischmann W., Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,				

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OM protein - protein search, using sw model

Run on: October 8, 2002, 15:05:27 ; Search time 42.5 Seconds
(without alignments)
938.247 Million cell updates/sec

Title: US-09-744-748-1

Perfect score: 1970

Sequence: 1 MTSISKGLRFLIVCIILG.....HVKRHQEVKSVGNLEKWFVN 359

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1970	100.0	359	21	Murine alpha-1,3-f
2	1961	99.5	359	21	Human alpha-1,3-fu
3	693.5	35.2	405	11	CDX, a MIIA involv
4	693.5	35.2	405	12	GDP-Fuc:beta-D-Gal
5	693.5	35.2	405	12	Protein 7.2 (1.3-f
6	693.5	35.2	405	13	Hela cell fucosylt
7	693.5	35.2	530	12	Protein 1 (1.3-fuc
8	689.5	35.0	405	15	A glycosyltransfer
9	689.5	35.0	405	18	Human alpha(1,3)-f
10	685.5	34.8	405	18	Human myeloid deri
11	679	34.5	360	18	Human chimeric fuc

12	678	34.4	360	18	AAW14514	Human chimeric fuc
13	677	34.4	361	18	AAW14530	Human chimeric fuc
14	676	34.3	361	18	AAW14520	Human chimeric fuc
15	675	34.3	361	18	AAW14517	Human chimeric fuc
16	674	34.2	360	18	AAW14516	Human chimeric fuc
17	672.5	34.1	359	18	AAW14523	Human chimeric fuc
18	672	34.1	360	18	AAW14526	Human chimeric fuc
19	672	34.1	496	15	AAW45938	A glycosyltransfer
20	671	34.1	361	18	AAW14519	Human chimeric fuc
21	670	34.0	361	12	AAW13749	GDP-Fuc:[beta-D-Ga
22	670	34.0	361	15	AAW45934	A glycosyltransfer
23	670	34.0	361	18	AAW23806	Human alpha 1,3/4
24	670	34.0	361	18	AAW14527	Human chimeric fuc
25	670	34.0	361	18	AAW13638	Human alpha(1,3/1,
26	670	34.0	361	22	AAW64452	Human Lewis enzyme
27	670	34.0	374	15	AAW45939	A glycosyltransfer
28	670	34.0	374	18	AAW13642	Human alpha(1,3)-f
29	665.5	33.8	359	15	AAW45933	Alpha-(1-3)Fuc-TV1
30	665.5	33.8	359	18	AAW14529	Human chimeric fuc
31	665.5	33.8	359	18	AAW13643	Human alpha(1,3)-f
32	664.5	33.7	359	18	AAW14524	Human chimeric fuc
33	663.5	33.7	360	18	AAW14528	Human chimeric fuc
34	663	33.7	361	18	AAW14518	Human chimeric fuc
35	661.5	33.6	360	18	AAW14521	Human chimeric fuc
36	660.5	33.5	359	18	AAW14522	Human chimeric fuc
37	659.5	33.5	359	18	AAW14525	Human chimeric fuc
38	658.5	33.4	359	18	AAW14531	Human chimeric fuc
39	657.5	33.4	360	18	AAW14512	Human chimeric fuc
40	656.5	33.3	360	18	AAW14513	Human chimeric fuc
41	625	31.7	342	15	AAW63215	Human alpha-1,3-fu
42	622	31.6	342	20	AAW27558	Human alpha1,3-fuc
43	608.5	30.9	350	18	AAW14532	Human chimeric fuc
44	583	29.6	342	18	AAW11820	Murine myeloid-lin
45	582	29.5	342	18	AAW26671	Mouse alpha-fucosy

ALIGNMENTS

```

RESULT 1
AAW80995
ID  AAW80995 standard; Protein; 359 AA.
XX
AC  AAW80995;
XX
XX  05-JUN-2000 (first entry)
DT
DE  Murine alpha-1,3-fucosyltransferase.
XX
KW  Alpha-1,3-fucosyltransferase; fucose; glycosylation; Lewis epitope;
KW  brain; kidney; recombinant expression; transgenic animal; knockout
KW  animal; FUC-TV; drug screening; inhibitor; potentiator; diagnosis;
KW  treatment; cancer; murine; mouse.
XX
OS  Mus sp.
XX
PN  WO200006708-A1.
XX
PD  10-FEB-2000.
XX
PF  29-JUL-1999; 99WO-JP04092.
XX
PR  29-JUL-1998; 98JP-0213823.
XX
PA  (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI  Narimatsu H, Kudo T, Sasaki K;
XX
DR  WPI; 2000-183120/16.
XX
DR  N-PSDB; AAW292645.
XX
PT  Alpha 1,3-fucosyltransferase generating Lewis x but not sialyl-Lewis x
    epitope and an antibody recognizing it useful for diagnosis of brain

```

PT animal; FUC-TIV; drug screening; inhibitor; potentiator; diagnosis;
 PS treatment; cancer; human.
 XX Homo sapiens.
 XX WO200006708-A1.
 XX 10-FEB-2000.
 XX 29-JUL-1999; 99WO-JP04092.
 XX 29-JUL-1998; 98JP-0213823.
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 XX Narimatsu H, Kudo T, Sasaki K;
 XX WPI; 2000-183120/16.
 XX N-PSDB; AA292646, AA292647.
 XX Alpha 1,3-fucosyltransferase generating Lewis x but not sialyl-Lewis x
 XX epitope and an antibody recognizing it useful for diagnosis of brain
 XX PT and kidney disease and cancer.
 XX PS Claim 2; Page 124-127; 172pp; Japanese.
 XX The invention relates to a novel alpha-1,3-fucosyltransferase which
 XX transfers a fucose moiety to galactosyl-beta-1-4-N-acetylglucosamine
 XX (generating the Lewis x or y epitope). It does not transfer a fucose
 XX moiety to alpha-2,3-sialyl-galactosyl-beta-1-4-N-acetylglucosamine
 XX and therefore does not generate the sialyl-Lewis x epitope. The
 XX invention also relates to DNA sequences encoding alpha-1,3-
 XX fucosyltransferase and expression vectors and host cells comprising these
 XX DNA sequences. The invention additionally encompasses the preparation of
 XX alpha-1,3-fucosyltransferase via the culture of transformed cells or by
 XX expression of the protein in a transgenic animal; antibodies which
 XX recognise alpha-1,3-fucosyltransferase; methods for screening potential
 XX inhibitors of potentiation of alpha-1,3-fucosyltransferase activity or
 XX expression; the preparation of compounds having fucose-containing sugar
 XX chains by use of the protein; and knockout non-human animals lacking
 XX alpha-1,3-fucosyltransferase. Alpha-1,3-fucosyltransferase has a similar
 XX substrate range to the known FUC-TIV and is expressed mainly in brain and
 XX kidney tissues. Alpha-1,3-fucosyltransferase, nucleotides which encode
 XX it, antibodies, potentiators and inhibitors may be used for the
 XX treatment and diagnosis of diseases of the brain and kidney, and of
 XX cancers. They may be used for the identification of substances
 XX which affect the activity or expression of alpha-1,3-fucosyltransferase;
 XX such substances may be used therapeutically. The knockout animals can
 XX be used to study the mechanisms of action and expression of alpha-1,3-
 XX fucosyltransferase. The present sequence represents murine
 XX alpha-1,3-fucosyltransferase.
 XX SQ Sequence 359 AA;

Query Match 100.0%; Score 1970; DB 21; Length 359;
 Best Local Similarity 100.0%; Pred. No. 9 5e-171;
 Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSTSGILRPFLIVCIILGCFMACLLIYIKPTNSWVSPMESASSVLKMKNFSTKTDY 60
 Db 1 MTSTSGILRPFLIVCIILGCFMACLLIYIKPTNSWVSPMESASSVLKMKNFSTKTDY 60

QY 61 FNETTLVWVWPPGQTFDLTSCQAMFNIQCHLTDRSLYKSHAVLIHHRDISWDLTNL 120
 Db 61 FNETTLVWVWPPGQTFDLTSCQAMFNIQCHLTDRSLYKSHAVLIHHRDISWDLTNL 120

QY 121 PQARPPFKQIWMNLESPTHTPKSGIEHLFNLTLTYRRSDIQVPYGLTVSTNPFVF 180
 Db 121 PQARPPFKQIWMNLESPTHTPKSGIEHLFNLTLTYRRSDIQVPYGLTVSTNPFVF 180

QY 181 EVPSKEKLVCMVWVSNWNPENHARVKYNNELSKSIEHTYQAFGEYVNDKNLIPTISTCKF 240
 Db 181 EVPSKEKLVCMVWVSNWNPENHARVKYNNELSKSIEHTYQAFGEYVNDKNLIPTISTCKF 240

QY 241 YLSPENSITKDYITEKLYNAFLAGSVPLVGPSPRENYENIPADSFTHVEDFNSPSELAK 300
 Db 241 YLSPENSITKDYITEKLYNAFLAGSVPLVGPSPRENYENIPADSFTHVEDFNSPSELAK 300

QY 301 YLKEVDKNNKLYLSYFNWRKDFTNLPRFWEHACLDHVKRHOEYKSVGNLEKFWFN 359
 Db 301 YLKEVDKNNKLYLSYFNWRKDFTNLPRFWEHACLDHVKRHOEYKSVGNLEKFWFN 359

RESULT 2
 AAY80996
 ID AAY80996 standard; Protein; 359 AA.
 XX
 AC AAY80996;
 XX
 DT 05-JUN-2000 (first entry)
 XX Human alpha-1,3-fucosyltransferase.
 DE Alpha-1,3-fucosyltransferase.
 XX Alpha-1,3-fucosyltransferase; fucose; glycosylation; Lewis epitope;
 KW brain; kidney; recombinant expression; transgenic animal; knockout

KW animal; FUC-TIV; drug screening; inhibitor; potentiator; diagnosis;
 KW treatment; cancer; human.
 XX Homo sapiens.
 XX WO200006708-A1.
 XX 10-FEB-2000.
 XX 29-JUL-1999; 99WO-JP04092.
 XX 29-JUL-1998; 98JP-0213823.
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 XX Narimatsu H, Kudo T, Sasaki K;
 XX WPI; 2000-183120/16.
 XX N-PSDB; AA292646, AA292647.
 XX Alpha 1,3-fucosyltransferase generating Lewis x but not sialyl-Lewis x
 XX epitope and an antibody recognizing it useful for diagnosis of brain
 XX PT and kidney disease and cancer.
 XX PS Claim 2; Page 124-127; 172pp; Japanese.
 XX The invention relates to a novel alpha-1,3-fucosyltransferase which
 XX transfers a fucose moiety to galactosyl-beta-1-4-N-acetylglucosamine
 XX (generating the Lewis x or y epitope). It does not transfer a fucose
 XX moiety to alpha-2,3-sialyl-galactosyl-beta-1-4-N-acetylglucosamine
 XX and therefore does not generate the sialyl-Lewis x epitope. The
 XX invention also relates to DNA sequences encoding alpha-1,3-
 XX fucosyltransferase and expression vectors and host cells comprising these
 XX DNA sequences. The invention additionally encompasses the preparation of
 XX alpha-1,3-fucosyltransferase via the culture of transformed cells or by
 XX expression of the protein in a transgenic animal; antibodies which
 XX recognise alpha-1,3-fucosyltransferase; methods for screening potential
 XX inhibitors of potentiation of alpha-1,3-fucosyltransferase activity or
 XX expression; the preparation of compounds having fucose-containing sugar
 XX chains by use of the protein; and knockout non-human animals lacking
 XX alpha-1,3-fucosyltransferase. Alpha-1,3-fucosyltransferase has a similar
 XX substrate range to the known FUC-TIV and is expressed mainly in brain and
 XX kidney tissues. Alpha-1,3-fucosyltransferase, nucleotides which encode
 XX it, antibodies, potentiators and inhibitors may be used for the
 XX treatment and diagnosis of diseases of the brain and kidney, and of
 XX cancers. They may be used for the identification of substances
 XX which affect the activity or expression of alpha-1,3-fucosyltransferase;
 XX such substances may be used therapeutically. The knockout animals can
 XX be used to study the mechanisms of action and expression of alpha-1,3-
 XX fucosyltransferase. The present sequence represents human
 XX alpha-1,3-fucosyltransferase.
 XX SQ Sequence 359 AA;

Query Match 99.5%; Score 1961; DB 21; Length 359;
 Best Local Similarity 99.2%; Pred. No. 6 2e-170;
 Matches 356; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTSTSGILRPFLIVCIILGCFMACLLIYIKPTNSWVSPMESASSVLKMKNFSTKTDY 60
 Db 1 MTSTSGILRPFLIVCIILGCFMACLLIYIKPTNSWVSPMESASSVLKMKNFSTKTDY 60

QY 61 FNETTLVWVWPPGQTFDLTSCQAMFNIQCHLTDRSLYKSHAVLIHHRDISWDLTNL 120
 Db 61 FNETTLVWVWPPGQTFDLTSCQAMFNIQCHLTDRSLYKSHAVLIHHRDISWDLTNL 120

QY 121 PQARPPFKQIWMNLESPTHTPKSGIEHLFNLTLTYRRSDIQVPYGLTVSTNPFVF 180
 Db 121 PQARPPFKQIWMNLESPTHTPKSGIEHLFNLTLTYRRSDIQVPYGLTVSTNPFVF 180

QY 181 EVPSKEKLVCMVWVSNWNPENHARVKYNNELSKSIEHTYQAFGEYVNDKNLIPTISTCKF 240
 Db 181 EVPSKEKLVCMVWVSNWNPENHARVKYNNELSKSIEHTYQAFGEYVNDKNLIPTISTCKF 240


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QY 69 WWPFGQTEDEL-----TSCQAMENIOGCHLTDRSLYKNKSHAVLIHHRDI-----SW----- 115
DB 69 WWPFGGRDSAPRPPPPCLRFNIGSCLRLTDRASTGEAQAVLFHHRDLVKGPDPWPPPW 128
QY 116 -----DLTNLPQO-----ARPPQKWIWMNLESPTHTP-QKSGIEHL 151
DB 129 GIOAHTAEVDLRVLYDEEAAAAEALATSSPRPPGQRMWMMNFESPSHSGLSLASNL 188
QY 152 FNLTLYRRSDIQVYGFELTVSTNPFVEVPS-----KEKLCVWVSNMNPESHARV 203
DB 189 FNWTLSTRADSDVPVPGYLYPRSHP--GDPPSGLAPPLSRKQGLVAVVSHWDERQARV 246
QY 204 KYNELSKSIEHTYGOAF-GEYVNDKNLIPTISTCKFYLSFENSHTKDYITEKLY-NAF 261
DB 247 RYIHQLSHQVTVDFGGRGQGPVPEIGLHTVARYKYFLAFENSQHLDYITEKLWRNAL 306
QY 262 LAGSPVVLGSPRENYENYIPADSFHVEDFNSPSELAKYLKEVDKNNKLYLSYFNWRKD 321
DB 307 LAGAVPVVLGPDPRANYERFVRGAFIHVDFFPSASSLASLYLLFLDRNPVAVRYRHFHRRS 366
QY 322 FTVNLPFWESHACLADHVKKRHOEY-KSVGNLEKWF 357
DB 367 YAVHITSFWDPEWCRVCOAVORAGDRPKSIRNLASMF 403

RESULT 5
AAR14404
ID AAR14404 standard; Protein; 405 AA.
XX AAR14404;
XX AC
XX DT 13-FEB-1992 (first entry)
XX DE Protein 7.2 (1.3-fucosyl transferase).
XX KW CDX; cell adhesion; ELAM1.
XX OS Homo sapiens.
XX PN W09116900-A.
XX PD 14-NOV-1991.
XX PF 26-OCT-1990; 90WO-US06198.
XX PR 27-APR-1990; 90WO-US02357.
XX PR 26-OCT-1990; 90WO-US06198.
XX PA (BIOJ ) BIOGEN INC.
XX PI Goelz SE, Hession CA;
XX DR WPI; 1991-353507/48.
XX DR N-PSDB; AAQ14382.
XX DNA sequences encoding 1,3-fucosyl transferase - used to develop
XX antiinflammatory therapy by inhibition of linking activity.
XX PS Claim 23; Fig 1; 38pp; English.
XX CC The sequence was deduced from CDX pCDM8 clone 7.2 and from a
XX portion of the 7.2 insert subcloned into the sequencing vector
XX CC PN11 to prepare pSQ19. The protein, a 1,3-fucosyl transferase is
XX CC a surface glycoprotein which is recognised by anti-CDX antibodies
XX CC and which binds to ELAM1. The sequence is identical to the portion
XX CC of protein 1 (encoded by clone 1; AAQ14383) from residue 126-530.
XX CC The two proteins may represent different transcripts from the same
XX CC DNA segment. The protein may be useful in the development of anti-
XX CC inflammatory or other therapies.
XX CC See also AAR14405.
XX Sequence 405 AA;
XX SQ

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Query Match 35.2%; Score 693.5; DB 12; Length 405;
Best Local Similarity 38.8%; Pred. No. 1.5e-54;
Matches 154; Conservative 59; Mismatches 109; Indels 75; Gaps 14;

QY 15 VCIIILGCFMAC--LLIYI----KPTNSWVFSMESASSVLKMKNEFFSTKTDYFNETTILV 68
DB 28 VCVLAAGATCTALITYACWGQLPLPWA-SPTPS-----RPGVLL 68
QY 69 WWPFGQTEDEL-----TSCQAMENIOGCHLTDRSLYKNKSHAVLIHHRDI-----SW----- 115
DB 69 WWPFGGRDSAPRPPPPCLRFNIGSCLRLTDRASTGEAQAVLFHHRDLVKGPDPWPPPW 128
QY 116 -----DLTNLPQO-----ARPPQKWIWMNLESPTHTP-QKSGIEHL 151
DB 129 GIOAHTAEVDLRVLYDEEAAAAEALATSSPRPPGQRMWMMNFESPSHSGLSLASNL 188
QY 152 FNLTLYRRSDIQVYGFELTVSTNPFVEVPS-----KEKLCVWVSNMNPESHARV 203
DB 189 FNWTLSTRADSDVPVPGYLYPRSHP--GDPPSGLAPPLSRKQGLVAVVSHWDERQARV 246
QY 204 KYNELSKSIEHTYGOAF-GEYVNDKNLIPTISTCKFYLSFENSHTKDYITEKLY-NAF 261
DB 247 RYIHQLSHQVTVDFGGRGQGPVPEIGLHTVARYKYFLAFENSQHLDYITEKLWRNAL 306
QY 262 LAGSPVVLGSPRENYENYIPADSFHVEDFNSPSELAKYLKEVDKNNKLYLSYFNWRKD 321
DB 307 LAGAVPVVLGPDPRANYERFVRGAFIHVDFFPSASSLASLYLLFLDRNPVAVRYRHFHRRS 366
QY 322 FTVNLPFWESHACLADHVKKRHOEY-KSVGNLEKWF 357
DB 367 YAVHITSFWDPEWCRVCOAVORAGDRPKSIRNLASMF 403

RESULT 6
AAR28840
ID AAR28840 standard; Protein; 405 AA.
XX AAR28840;
XX AC
XX DT 05-APR-1993 (first entry)
XX DE HeLa cell fucosyltransferase enzyme.
XX KW glycosyltransferase; galactosyltransferase; sialyltransferase;
XX fucosyltransferase; membrane bound; ss.
XX OS Homo sapiens.
XX PN GB2256197-A.
XX PD 02-DEC-1992.
XX PF 14-APR-1992; 92GB-0008211.
XX PR 31-MAY-1991; 91EP-0810414.
XX PR 04-MAR-1992; 92EP-0810167.
XX PR 14-APR-1992; 92GB-0008211.
XX PA (CIBA ) CIBA GEIGY AG.
XX PI Berger EG, Meyhack B, Watzele G, Watzele M, Berger E;
XX DR WPI; 1992-401159/49.
XX DR N-PSDB; AAQ31434.
XX PT Glycosyltransferase prodn. process - includes transforming yeast
XX cells with expression cassettes contg. mammalian coding sequences
XX controlled by yeast promoters
XX PS Claim 16; Page 43; 65pp; English.
XX CC This sequence represents a fucosyltransferase enzyme from HeLa cells.

```



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PN WO9640881-A1.
XX
PD 19-DEC-1996.
XX
PF 08-MAY-1996; 96WO-US06427.
XX
PR 07-JUN-1995; 95US-0483151.
XX
PA (GEO ) GEN HOSPITAL CORP.
XX
XX Holgersson J, Seed B;
XX WPI; 1997-108639/10.
DR N-PSDB; AAT58506.
DR
XX
XX New murine alpha-(1,3)-fucosyltransferase - for fucosylating an
PT antibody to protect mammals against e.g. septic shock or septicaemia
PT
XX
XX Claim 17; Fig 6B; 58pp; English.
XX
XX Introduction of human myeloid cell-specific fucosyltransferase
CC Fuc-TIV (AAW11821) into a murine cell line results in the appearance
CC of a fucosylated glycan pattern similar to that found on human
CC neutrophils and monocytes. Murine cells expressing human Fuc-TIV
CC show enhanced adhesion to E-selectin fusion proteins, indicating
CC that Fuc-TIV is involved in human granulocyte extravasation. Host
CC cells (e.g. 32B cl3 or human 293 cells) transformed with DNA (see
CC also AAT59506) encoding Fuc-TIV and DNA encoding murine alpha-(1,3)-
CC fucosyltransferase (see also AAW11820), can be used to fucosylate
CC ADP-antibody, IgG or IGM for use in protecting an animal against an
CC adverse immune reaction, esp. septic shock or septicaemia.
XX
XX Sequence 405 AA;
XX
XX Query Match 34.8%; Score 685.5; DB 18; Length 405;
XX Best Local Similarity 38.3%; Pred. No. 7.9e-54;
XX Matches 152; Conservative 60; Mismatches 110; Indels 75; Gaps 14;
XX
QY 15 VCILGCFMAC--LLIYI----KPTNSWFPSPMESASSVLKMNFFSTKTDYFNETHIV 68
DB 28 VCVLAAAGLCTALITYACWGLPLFWA-SPTPS-----RPVGVLL 68
QY 69 WVPFQGTDFL----TSCQAMENIOGCHLTDRSLYNKSHAVLIHHRDI-----SW---- 115
DB 69 WVEPFGAISAPRPPDPCRLRNFISGRLTDRASYGEAQVLFHHRDLVKGGPDWPPPW 128
QY 116 -----DLTNLPQ-----ARPPFQKWIWMNLESPTHTP-QKSGIEHL 151
DB 129 GIOHTAAEVDLRLVDYEEAAAAAALATSSPRPRAKRWMMFSPSHSGPLRLSNL 188
QY 152 FNTLTLYRRSDIOVPYGFITVSTNPFVEVPS-----KEKLCVWVSVNNPHEARV 203
DB 189 FNNLTLYRADSDVFPYGYLYPRSHP--GDPPSGLAPPLSRKQGLVAVVSHWDERQARV 246
QY 204 KYNELSKSIEIHTYGOAF-GEVVDKNLPTLTSTCKFVLSFENSJHKDYITEKLY-NAF 261
DB 247 RYTHQLSQHVTVDVFGGGPGQVPEIGLHTVARFYKFLAFENSQHLDYITEKLRNAL 306
QY 262 LAGSVPVVLGSPRENTENYIPADSFHVEDFNSPSELAKYLKEVDKNNKLYLSYFNWRKD 321
DB 307 LACAVPVVLGPDRAHYERFVRGAFIHVDFFPSSASLASVLLFLDRNPAYVRYRHFHRRS 366
QY 322 FTVNLPFRFESHACLADHVKRRHQEY-KSVGNLEKWF 357
DB 367 YAVHITSFWDPEWCRCVQAVORAGDRPKSIRNLASF 403
RESULT 11
AAW14515
ID AAW14515 standard; Protein; 360 AA.
XX
AC AAW14515;
XX
```

```
DT 19-JUN-1997 (first entry)
XX Human chimeric fucosyltransferase Fuc-TC4.
DE
XX
KW Alpha(1,3/1,4)-fucosyltransferase; Lewis enzyme; Fuc-TIII;
KW alpha(1,3)-fucosyltransferase; Fuc-TVI; glycosylation;
KW oligosaccharide; Fuc-TC4.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Region 1..159
FT /label= Fuc-TIV
FT /note= "amino acids 1-159 of Fuc-TIV"
FT 160..360
FT /label= Fuc-TIII
FT /note= "amino acids 161-361 of Fuc-TIII"
FT 46
FT Modified-site /label= Glycosylation
FT 91
FT Modified-site /label= Glycosylation
FT 153
FT Modified-site /label= Glycosylation
XX
PN WO9709421-A1.
XX
XX 13-MAR-1997.
PD
XX
XX 06-SEP-1996; 96WO-US13816.
PF
XX
XX 08-SEP-1995; 95US-0525058.
PR
XX
XX (UNMI ) UNIV MICHIGAN.
XX
XX Legault DJ, Lowe JB;
XX WPI; 1997-192897/17.
XX
XX New recombinant fucosyltransferase proteins - useful for modifying
XX cell surface oligosaccharide structures
XX
XX Claim 1; Refer to Page 294; 329pp; English.
XX
XX Chimeric fucosyltransferases Fuc-TC1 to Fuc-TC21 (AAW14512-31)
XX comprise portions of the human GDP-Fuc:(beta-D-Gal(1,4/1,3))-D-
XX GlcNAc(Glc) alpha(1,3/1,4)-fucosyltransferase (Fuc-TIII, Lewis
XX enzyme) (AAW13638) and portions of the GDP-Fuc:beta-D-Gal(1,4)-D-
XX GlcNAc alpha(1,3)-fucosyltransferase (Fuc-TVI) (AAW13643). They are
XX obtd. by cassette mutagenesis of Fuc-TIII and Fuc-TVI nucleic acids
XX (AAT61675, AAT61680) and expression in transformed host cells. The
XX chimeric fucosyltransferases can be used to modify cell surface
XX oligosaccharide structures.
XX
XX Sequence 360 AA;
XX
XX Query Match 34.5%; Score 679; DB 18; Length 360;
XX Best Local Similarity 43.1%; Pred. No. 2.6e-53;
XX Matches 134; Conservative 61; Mismatches 104; Indels 12; Gaps 8;
XX
QY 55 STKTDYFNETHIVWVPFQGTDFLTSCQAMF-NIOGCHLTDRSLYNKSHAVLIHHRDI 113
DB 53 STGTPAHSPLIILLWTWFPFNKPIALPCSEMPVPGTADCNITADRKVKVQADAVIVHREV 112
QY 114 SWD-LTNLPQARPPFPQKWIWMNLESPTHTPQKSGIEHLNLTLYRRSDIOVPYGFIT 172
DB 113 MYNPSAQLPRSPRQGRQGWIFWFSMESPSHCWQKAMDGYENLTWSYRSDSDITFPYGLW 172
QY 173 V-STNPF--VFEPVPSKEKLCVWVSVNNPHEARVKNYNNELSKSIEIHTYGOAFGEYNDK 229
DB 173 PWSGQPAHPPLNLAKTLEWAVAVSNWPKDPSARVRYQSLQAHKLKVDVYGRSH-KPLPKG 231
QY 230 NLIPTISTCKFVLSFENSJHKDYITEKLY-NAFLAGSVPVVLGSPRENTENYIPADSFTH 268
XX
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Db 232 TMMETLSRYKYLAFENSLHPDYITEKLRNALAEAWVVPVGLPSRNYERFLPPDAFIH 291
QY 289 VEDFNSPSELAKYLKEVDKNNKLYSYFNWRKDFTVNLPR--FWESHACIACDVKRHOE 346
   || || || || || || || || || || || || || || || || || || || || ||
Db 292 VDDFQSPKDLARYLQELDKDHARYLSYFRWRETLR---PRSFSWALDFCKACWKLOQESR 348
QY 347 YKSVGNLEKWF 357
   || || || || || || || || || || || || || || || || || || || || ||
Db 349 YQTVRSIAAWF 359

RESULT 12
AAW14514
ID AAW14514 standard; Protein; 360 AA.
XX
AC AAW14514;
XX
DT 19-JUN-1997 (first entry)
XX
DE Human chimeric fucosyltransferase Fuc-TC3.
XX
KW Alpha(1,3/1,4)-fucosyltransferase; Lewis enzyme; Fuc-TIII;
KW alpha(1,3)-fucosyltransferase; Fuc-TVI; glycosylation;
KW oligosaccharide; Fuc-TC3.
XX
OS Synthetic.
XX
FH Key
FT 1..300 Location/Qualifiers
FT Region
FT /label= Fuc-TIV
FT /note= "amino acids 1-300 of Fuc-TIV"
FT Region
FT 301..360
FT /label= Fuc-TIII
FT /note= "amino acids 302-361 of Fuc-TIII"
FT Modified-site
FT 46
FT /label= Glycosylation
FT Modified-site
FT 91
FT /label= Glycosylation
FT Modified-site
FT 153
FT /label= Glycosylation
FT 154
FT /label= Glycosylation
XX
PN WO9709421-A1.
XX
PD 13-MAR-1997.
XX
PF 06-SEP-1996; 96WO-US13816.
XX
PR 08-SEP-1995; 95US-0525058.
XX
PA (UNMI ) UNIV MICHIGAN.
XX
PI Legault DJ, Lowe JB;
XX
DR WPI; 1997-192897/17.
XX
PT New recombinant fucosyltransferase proteins - useful for modifying
PT cell surface oligosaccharide structures
XX
PS Claim 1; Refer to Page 294; 329pp; English.
XX
CC Chimeric fucosyltransferases Fuc-TC1 to Fuc-TC21 (AAW14512-31)
CC comprise portions of the human GDP-Fuc:(beta-D-Gal(1,4/1,3))-D-
CC GlcNAc(6/6) alpha(1,3/1,4) fucosyltransferase (Fuc-TIII, Lewis
CC enzyme) (AAW13638) and portions of the GDP-Fuc:(beta-D-Gal(1,4)-D-
CC GlcNAc alpha(1,3) fucosyltransferase (Fuc-TVI) (AAW13643). They are
CC obcd; by cassette mutagenesis of Fuc-TIII and Fuc-TVI nucleic acids
CC (AA61675, AA61680) and expression in transformed host cells. The
CC chimeric fucosyltransferases can be used to modify cell surface
CC oligosaccharide structures.
XX
SQ Sequence 360 AA;

Query Match 34.4%; Score 678; DB 18; Length 360;

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Best Local Similarity 43.1%; Pred. No. 3.2e-53;
Matches 134; Conservative 60; Mismatches 105; Indels 12; Gaps 8;
QY 55 STKTDYFNETTILVWVPFGQTFDLTSCQAMF-NIOGCHLTTRSLYKNSHAVLIHHRDI 113
   || || || || || || || || || || || || || || || || || || || || ||
Db 53 STGTPAHISIPILLTLTWPFNKPIALPRCSEMVPGTADCNITADKVVYPQADAVIVHREV 112
QY 114 SWD-LTNLPOQARPPFOKWIWMNLESPTHTPOKSGIEHLENLTLYRRSDIOVPYGFELT 172
   || || || || || || || || || || || || || || || || || || || || ||
Db 113 MYNPSAQLPRSPRQGORWIFSMESPSHCWOLKAMDGYENLTMSYSDSDITFTYGWLE 172
QY 173 V-STNPF--VFEVPSKEKLYCWVWSNMNDEHARVKYNNLSKSIETHYCOAFGEVYNDK 229
   || || || || || || || || || || || || || || || || || || || || ||
Db 173 PWSGQPAHPPLNLSAKTELVAWVSNMGPNRSARVRYTQSLQHLKVDVYGRSH-KPLDQ 231
QY 230 NLIPTISTCKFYLSFENSIIHKDYITEKLY-NAFLAGSVPVVGLPSRNYENYIPADSFH 288
   || || || || || || || || || || || || || || || || || || || || ||
Db 232 TMMETLSRYKYLAFENSLHPDYITEKLRNALAEAWVVPVGLPSRNYERFLPPDAFIH 291
QY 289 VEDFNSPSELAKYLKEVDKNNKLYSYFNWRKDFTVNLPR--FWESHACIACDVKRHOE 346
   || || || || || || || || || || || || || || || || || || || || ||
Db 292 VDDFQSPKDLARYLQELDKDHARYLSYFRWRETLR---PRSFSWALDFCKACWKLOQESR 348
QY 347 YKSVGNLEKWF 357
   || || || || || || || || || || || || || || || || || || || || ||
Db 349 YQTVRSIAAWF 359

RESULT 13
AAW14530
ID AAW14530 standard; Protein; 361 AA.
XX
AC AAW14530;
XX
DT 19-JUN-1997 (first entry)
XX
DE Human chimeric fucosyltransferase Fuc-TC19.
XX
KW Alpha(1,3/1,4)-fucosyltransferase; Lewis enzyme; Fuc-TIII;
KW alpha(1,3)-fucosyltransferase; Fuc-TVI; glycosylation;
KW oligosaccharide; Fuc-TC19.
XX
OS Synthetic.
XX
FH Key
FT 1..99 Location/Qualifiers
FT Region
FT /label= Fuc-TIII
FT /note= "amino acids 1-99 of Fuc-TIII"
FT Region
FT 100..160
FT /label= Fuc-TVI
FT /note= "amino acids 99-159 of Fuc-TVI"
FT Region
FT 161..361
FT /label= Fuc-TIII
FT /note= "amino acids 161-361 of Fuc-TIII"
FT Modified-site
FT 154
FT /label= Glycosylation
XX
PN WO9709421-A1.
XX
PD 13-MAR-1997.
XX
PF 06-SEP-1996; 96WO-US13816.
XX
PR 08-SEP-1995; 95US-0525058.
XX
PA (UNMI ) UNIV MICHIGAN.
XX
PI Legault DJ, Lowe JB;
XX
DR WPI; 1997-192897/17.
XX
PT New recombinant fucosyltransferase proteins - useful for modifying
PT cell surface oligosaccharide structures

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```

XX PS Claim 1; Refer to Page 298; 329pp; English.
XX PR
XX CC Chimeric fucosyltransferases Fuc-TC1 to Fuc-TC21 (AAW14512-31)
XX CC comprise portions of the human GDP-Fuc:(beta-D-Gal(1,4/1,3))-D-
XX CC GlcNAc(Glc) alpha(1,3/1,4)-fucosyltransferase (Fuc-TIII, Lewis
XX CC enzyme) (AAW13638) and portions of the GDP-Fuc:beta-D-Gal(1,4)-D-
XX CC GlcNAc alpha(1,3)fucosyltransferase (Fuc-TVI) (AAW13643). They are
XX CC obtd. by cassette mutagenesis of Fuc-TIII and Fuc-TVI nucleic acids
XX CC (AAW1675, AAW1680) and expression in transformed host cells. The
XX CC chimeric fucosyltransferases can be used to modify cell surface
XX CC oligosaccharide structures.
XX SQ Sequence 361 AA;

Query Match 34.4%; Score 677; DB 18; Length 361;
Best Local Similarity 44.0%; Pred. No. 4e-53;
Matches 132; Conservative 59; Mismatches 97; Indels 12; Gaps 8;

QY 66 ILVWVPEFGTDLTSCQAMF-NIQGCHLTDRSLYNKSHAVLIHHRDISWD-LTNLPQQ 123
DB 65 ILLWTWPFHPVALSRCEMVPGTADCHITADRKVPQADAVIHHKVENYNSAQLPRS 124

QY 124 ARPPFQKIWNLESPTHTPKSGIEHLENLTLTYRSDSIQVPGFLTV-STNPF--VF 180
DB 125 PRQGGQRIWFSPMESPSCHQWLKAMDGYFNLTMSYRSDSDIFTYPGWLEPWSGQPAHPPL 184

QY 181 EVPSKEKLVCVWVSNMNNPEHARVYKYNELSKSIEHTYGOAFGEYVNDKNLIPTISTCKF 240
DB 185 NLSAKTELAVAWVSNMKNPKDSARVYQSLQALHKVDVYGRSH-KPLPKGTMMETLSRYKF 243

QY 241 YLSFENSIHKDYITEKLY-NAFLAGSVVPVVLGSPRENYENYIPADSFHVEDNSPELA 299
DB 244 YLAFENSLHPDYITEKLWRNALAWAVPVVLGSPRSNYERFLPPDPAFIHVDDFQSPKDLA 303

QY 300 KYLKEVDKNNKLYSFNWRKDTVNLPR--FWESHACLACDHVKRHOEYKSVGNLEKWF 357
DB 304 RYLQELDKDHARYLSYFRWRETLR---PRSFSWALDFCKACWKLOQESRYQTVRSIAW 360

RESULT 14
AAW14520
ID AAW14520 standard; Protein; 361 AA.
XX
XX AC AAW14520;
XX
XX DT 19-JUN-1997 (first entry)
XX
XX DE Human chimeric fucosyltransferase Fuc-TC9.
XX
XX KW Alpha(1,3/1,4)-fucosyltransferase; Lewis enzyme; Fuc-TIII;
XX KW alpha(1,3)-fucosyltransferase; Fuc-TVI; glycosylation;
XX KW oligosaccharide; Fuc-TC9.
XX
XX OS Synthetic.
XX
XX FH Key
XX FT Region
XX FT 1..130
XX FT /label= Fuc-TIII
XX FT /note= "amino acids 1-130 of Fuc-TIII"
XX FT Region
XX FT 131..160
XX FT /label= Fuc-TVI
XX FT /note= "amino acids 130-159 of Fuc-TVI"
XX FT Region
XX FT 161..361
XX FT /label= Fuc-TIII
XX FT /note= "amino acids 161-361 of Fuc-TIII"
XX FT Modified-site
XX FT 154
XX FT /label= Glycosylation
XX
XX PN WO9709421-A1.
XX
XX PD 13-MAR-1997.
XX
XX FH Key

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PF 06-SEP-1996; 96WO-US13816.
XX
XX PR 08-SEP-1995; 95US-0525058.
XX
XX PA (UNMI ) UNIV MICHIGAN.
XX
XX PI Legault DJ, Lowe JB;
XX
XX WPI; 1997-192897/17.
XX
XX PT New recombinant fucosyltransferase proteins - useful for modifying
XX PT cell surface oligosaccharide structures
XX
XX PS Claim 1; Refer to Page 295; 329pp; English.
XX
XX CC Chimeric fucosyltransferases Fuc-TC1 to Fuc-TC21 (AAW14512-31)
XX CC comprise portions of the human GDP-Fuc:(beta-D-Gal(1,4/1,3))-D-
XX CC GlcNAc(Glc) alpha(1,3/1,4)-fucosyltransferase (Fuc-TIII, Lewis
XX CC enzyme) (AAW13638) and portions of the GDP-Fuc:beta-D-Gal(1,4)-D-
XX CC GlcNAc alpha(1,3)fucosyltransferase (Fuc-TVI) (AAW13643). They are
XX CC obtd. by cassette mutagenesis of Fuc-TIII and Fuc-TVI nucleic acids
XX CC (AAW1675, AAW1680) and expression in transformed host cells. The
XX CC chimeric fucosyltransferases can be used to modify cell surface
XX CC oligosaccharide structures.
XX SQ Sequence 361 AA;

Query Match 34.3%; Score 676; DB 18; Length 361;
Best Local Similarity 43.8%; Pred. No. 4.9e-53;
Matches 133; Conservative 56; Mismatches 95; Indels 20; Gaps 9;

QY 66 ILVWVPEFGTDLTSCQAMF-NIQGCHLTDRSLYNKSHAVLIHHRDISWDL-----TN 119
DB 65 ILLWTWPFHPVALSRCEMVPGTADCHITADRKVPQADTVIVHH---WDIMSNPKSR 120

QY 120 LPQARPPFQKIWNLESPTHTPKSGIEHLENLTLTYRSDSIQVPGFLTV-STNPF 178
DB 121 LPSPRQGGQRIWFSPMESPSCHQWLKAMDGYFNLTMSYRSDSDIFTYPGWLEPWSGQPA 180

QY 179 --VFEVPSKEKLVCVWVSNMNNPEHARVYKYNELSKSIEHTYGOAFGEYVNDKNLIPTIS 236
DB 181 HPPLNLSAKTELAVAWVSNMKNPKDSARVYQSLQALHKVDVYGRSH-KPLPKGTMMETLS 239

QY 237 TCKFYLSFENSIHKDYITEKLY-NAFLAGSVVPVVLGSPRENYENYIPADSFHVEDNSP 295
DB 240 RYKELYAFENSLHPDYITEKLWRNALAWAVPVVLGSPRSNYERFLPPDPAFIHVDDFQSP 299

QY 296 SELAKYLKEVDKNNKLYSFNWRKDTVNLPR--FWESHACLACDHVKRHOEYKSVGNL 353
DB 300 KDLARYLQELDKDHARYLSYFRWRETLR---PRSFSWALDFCKACWKLOQESRYQTVRSI 356

QY 354 EKWF 357
DB 357 AAWF 360

RESULT 15
AAW14517
ID AAW14517 standard; Protein; 361 AA.
XX
XX AC AAW14517;
XX
XX DT 19-JUN-1997 (first entry)
XX
XX DE Human chimeric fucosyltransferase Fuc-TC6.
XX
XX KW Alpha(1,3/1,4)-fucosyltransferase; Lewis enzyme; Fuc-TIII;
XX KW alpha(1,3)-fucosyltransferase; Fuc-TVI; glycosylation;
XX KW oligosaccharide; Fuc-TC6.
XX
XX OS Synthetic.
XX
XX FH Key

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Job time : 43.5 secs

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FT Region 1..70
FT /label= Fuc-TIII
FT /note= "amino acids 1-70 of Fuc-TIII"
FT 71..86
FT /label= Fuc-TVI
FT /note= "amino acids 70-85 of Fuc-TVI"
FT 87..361
FT /label= Fuc-TIII
FT /note= "amino acids 87-361 of Fuc-TIII"
FT 154
FT /label= Glycosylation
XX
XX WO9709421-A1.
XX
XX 13-MAR-1997.
XX
XX 06-SEP-1996; 96WO-US13816.
XX
XX 08-SEP-1995; 95US-0525058.
XX
XX (UNWI ) UNIV MICHIGAN.
XX
XX Legault DJ, Lowe JB;
XX
XX WPI; 1997-192897/17.
XX
XX New recombinant fucosyltransferase proteins - useful for modifying
XX cell surface oligosaccharide structures
XX
XX Claim 1; Refer to Page 295; 329pp; English.
XX
XX Chimeric fucosyltransferases Fuc-TC1 to Fuc-TC21 (AAW14512-31)
XX comprise portions of the human GDP-Fuc:(beta-D-Gal(1,4/1,3))-D-
XX GlcNAc(Glc) alpha(1,3/1,4)-fucosyltransferase (Fuc-TIII, Lewis
XX enzyme) (AAW13638) and portions of the GDP-Fuc:(beta-D-Gal(1,4)-D-
XX GlcNAc alpha(1,3)fucosyltransferase (Fuc-TVI) (AAW13643). They are
XX obtd. by cassette mutagenesis of Fuc-TIII and Fuc-TVI nucleic acids
XX (AAW61675, AAW61680) and expression in transformed host cells. The
XX chimeric fucosyltransferases can be used to modify cell surface
XX oligosaccharide structures.
XX
XX Sequence 361 AA;

Query Match 34.3%; Score 675; DB 18; Length 361;
Best Local Similarity 43.4%; Pred. No. 6,le-53;
Matches 132; Conservative 54; Mismatches 98; Indels 20; Gaps 9;

Qy 66 ILVWVWPGQFTDLSQAMF-NIQGCHLTDRSLYKSHAVLIHHRDISWDL-----TN 119
Db ||| ||| : | | | ||| ||| : | | | ||| : | | | ||| :
Qy 120 LPOQARPPQKWIWNLESPTHTPKSGIEHLENTLTLYRRSDIQVPGFLTV-STNPF 178
Db || || ||| ||| : | | | ||| ||| : | | | ||| ||| : |
Qy 121 LPPSPRQGRWIWFNLEPPPCQHLEALDRYFNLTMSYRSDSDIFTPGWLEPWSGQA 180
Db || ||| ||| : | | | ||| ||| : | | | ||| ||| : |
Qy 179 --VEEVPSEKELVCWVYNNWNPHEHARVYKYNELSKSIEIHTYQAFGEYVNDKNLIPTIS 236
Db : | : | | | | : | | | | | : | | | | | : | | | | | :
Qy 181 HPPLNLSAKTELVAWAVSNWPKPSARVRYQSLQAHLEKVDVYGRSH-KPLPKGTMMETLS 239
Db : | : | | | | : | | | | | : | | | | | : | | | | | :
Qy 237 TCKEYLPENSIEHKDYTEKLY-NAFLAGSVPVVLGSPRENYENYIPADSFHVEDENSP 295
Db ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Qy 240 RYKYLAFENSLHPDYITEKLRNLEAWAVPVVLGSPRSNYERFLPDAFIHVDDEQSP 299
Db ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Qy 296 SELAKYLEVDKNNKLYLNFNWKDFTVNLPR--FWESHACIACDVKHKHOKYKSGVNL 353
Db : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Qy 354 EKWF 357
Db ||
Qy 357 AAWF 360
Db ||

Search completed: October 8, 2002, 16:52:16
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 8, 2002, 16:34:47 ; Search time 15.5 Seconds
(without alignments)
2225.553 Million cell updates/sec

Title: US-09-744-748-1
Perfect score: 1970
Sequence: 1 WTSTSGILRFLIVCIILG.....HVKRHOEYKSVGNLEKWFVN 359

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR71:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	706	35.8	433	2 A57596	alpha-1,3-fucosyl
2	698	35.4	400	2 JC4591	alpha-1,3-fucosyl
3	693.5	35.2	405	2 B36340	alpha(1,3)-fucosyl
4	670	34.0	361	2 A36669	galactoside 3(4)-L
5	670	34.0	374	2 A42270	alpha(1,3) fucosyl
6	665.5	33.8	359	2 A45156	alpha-(1,3)-fucosyl
7	657	33.4	365	2 S53498	alpha(1,3/4)-fucosyl
8	650	33.0	364	2 I39048	alpha(1,3) fucosyl
9	622	31.6	342	2 A54057	alpha(1,3)-fucosyl
10	478.5	24.3	304	2 I39049	alpha(1,3) fucosyl
11	307	15.6	414	2 T15270	hypothetical prote
12	304	15.4	1652	2 T16799	hypothetical prote
13	285.5	14.5	451	2 T23491	hypothetical prote
14	227.5	11.5	393	2 H96742	hypothetical prote
15	204.5	10.4	513	2 F96533	probable fucosyltr
16	156.5	7.9	183	2 C97832	alpha-(1,3)-fucosyl
17	154.5	7.8	346	2 T44327	hypothetical prote
18	133.5	6.8	425	2 C64567	fucosyltransferase
19	133	6.8	436	2 G71862	alpha-(1,3)-fucosyl
20	133	6.8	454	2 B71914	alpha(1,3)-fucosyl
21	131.5	6.7	476	2 C64601	fucosyltransferase
22	124.5	6.3	876	2 S71277	serine/threonine-s
23	124.5	6.3	876	2 D85350	hypothetical prote
24	115.5	5.9	682	2 F81332	probable periplasm
25	114	5.8	1088	2 T41671	hypothetical prote
26	108	5.5	2628	2 S59413	probable membrane
27	105	5.3	537	2 T21823	hypothetical prote
28	104	5.3	747	2 T33488	hypothetical prote
29	102	5.2	2059	2 T41933	large legument pro

30	100.5	5.1	382	2 T29554	hypothetical prote
31	99.5	5.1	789	2 G90587	lipoprotein [impor
32	99	5.0	2028	2 T08025	DNA-directed RNA p
33	99	5.0	4550	2 T18440	hypothetical prote
34	98	5.0	441	2 F84560	purple acid phosph
35	98	5.0	526	2 F82873	hypothetical prote
36	97.5	4.9	335	2 AD1880	hypothetical prote
37	97.5	4.9	354	2 B97003	spermidine/putresc
38	97	4.9	408	2 T47585	hypothetical prote
39	97	4.9	1253	2 T40302	hypothetical prote
40	96.5	4.9	530	2 G71157	hypothetical prote
41	96.5	4.9	759	2 I38593	fibroblast activat
42	96	4.9	321	2 S54403	1-phosphatidylinos
43	96	4.9	566	2 JH0218	cellulase (EC 3.2.
44	96	4.9	1092	1 S37676	glutamate dehydrog
45	95.5	4.8	370	2 JC7591	spinal cord-derive

ALIGNMENTS

RESULT 1

A57596
alpha-1,3-fucosyltransferase Fuc-TIV (EC 2.4.1.-) - mouse
N:Alternate names: ELAM-1 ligand fucosyltransferase homolog
C:Species: Mus musculus (house mouse)
C:Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 11-Jan-2000
C:Accession: A57596
R:Gersten, K.M.; Natsuka, S.; Trinchera, M.; Petryniak, B.; Kelly, R.J.; Hiraiwa, N.;
J. Biol. Chem. 270, 25047-25056, 1995
A:Title: Molecular cloning, expression, chromosomal assignment, and tissue-specific e
rase.
A:Reference number: A57596; MUID:96027607
A:Accession: A57596
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-433 <ER>
A:Cross-references: GB:U33457; NID:gl039426; PTDN:AAC52269.1; PID:gl039427
C:Superfamily: galactoside 3(4)-L-fucosyltransferase
C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 35.8%; Score 706; DB 2: Length 433;
Best Local Similarity 42.7%; Pred. No. 9.4e-46;
Matches 146; Conservative 48; Mismatches 96; Indels 52; Gaps 8;

QY	66	ILVVMWPF-----GQTFDLTSCQAMFNIGQCHLTDRSLYKNSHAVLIHRDISWDLTNLP	121
DB	92	VLLWEPFRGCGYPKSPDCLRFNISGCRLLTDRAAYGEAQAVLFHRLDYKELHDWP	151
QY	122	QQ-----ARPPFQKWMNLSPTHTPKSG	147
DB	152	PPWGARERTDKALVLRVDFDQEGAVTLTGKALETVGSRPPCQRVMWVNFESPSHTPLRG	211
QY	148	I-EHLNLTLYRRSDIQVPGFLVTSTNPFVFEVS-----KEKLVGVVSWNWP	198
DB	212	LAKDLNWTLSYSTDVFPYGLYSRSDP--TEQPSGLGPGQLARRKGLVAVWVSWNE	269
QY	199	EHARVYNNELSKSIEHTYQCAF-GEYVNDKNLPIPTISCKFVLSFENSITKDYITEKL	257
DB	270	HQARVRYHQLSRHVSVDVFGRTGPRVPAIGLLHTVARYKFLAFENSRHVDYITEKL	329
QY	258	Y-NAFLAGSVPVVLGSPRENYIIPADSIHVEDFNPSSELAKYLKEVDKNKLYLSYF	316
DB	330	WRNAFLAGAVPVVLGPDRAHYERFVPRGAFIHVDVDFPNAASLAAYLLFLDRNVAVRYRF	389
QY	317	NWRKDTVNLPRWFESHACLACDHVKRH-QEYKSVGNLEKWF	357
DB	390	RWRSEAVHITSEWDEQWCRCTQAVOTSGDQPKSIHNLADWF	431

RESULT 2

JC4591
alpha-1,3 fucosyltransferase (EC 2.4.1.-) - mouse

A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-240, 'D', 242-400 <KUN>
 A:Cross-references: GB:565161; NID:g239005; PID:AAB20349.1; PID:g239006
 C:Genetics:
 A:Gene: GDB:FUT4; CD15; FCU3A; FUC-TIV
 A:Cross-references: GDB:1315

residues: 1-361 <RUK>
 residue type: mKNA
 cross-references: GB:X53578; NID:q28529; PIDN:CAA37641.1; PTD:q28530
 Ameron, H.S.; Szczepanlak, D.; Weston, B.W.
 J Biol. Chem. 270, 20112-20122, 1995

residues: 1-361 <RUK>
 residue type: mKNA
 cross-references: GB:X53578; NID:q28529; PIDN:CAA37641.1; PTD:q28530
 Ameron, H.S.; Szczepaniak, D.; Weston, B.W.
 J Biol. Chem. 270, 20112-20122, 1995

J. Biol. Chem. 270, 20112-20122, 1995

A>Title: Expression of human chromosome 19p alpha(1,3)-fucosyltransferase genes in no
A:Reference number: I39043; MUID:95378269

A:Accession: I39046

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-374 <RES>

A:Cross-references: EMBL:U27329; NID:g967194; PIDN:AAC50188.1; PID:g967195

A:Accession: I39047

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-374 <RE2>

A:Cross-references: EMBL:U27330; NID:g967196; PIDN:AAC50189.1; PID:g967197

C:Genetics:

A:Gene: GDB:FUT5

A:Cross-references: GDB:I31644; OMIM:136835

A:Map position: 19p13.3-19p13.3

C:Superfamily: galactoside 3(4)-L-fucosyltransferase

Query Match 34.0%; Score 670; DB 2; Length 374;
Best Local Similarity 44.0%; Pred. No. 4.le-43;
Matches 132; Conservative 57; Mismatches 99; Indels 12; Gaps 8;

Qy 66 ILVVWPFQGTFDLTSCQMF-NIQGCHLTDRSLYNKSHAVLIHHRDISWD-LTNLPQQ 123
||| ||| | | : |:| |:| :|:||||| :| :|
Db 78 ILLTWFPNTFVALPRCSMEVPGAADCNITADSSVPQDAVIYHHVDIMYPNSANLPPP 137
||| ||| | | : |:| |:| :|:||||| :| :|
Qy 124 ARPPFQKIWMNNLSPTHTPQKSIEHLNLTLTYRRDSIOVPYGFLTV-STNPFF--VF 180
||| ||| :|:||||| :|:||||| :|:||||| :|
Db 138 TRPOGQRWIWFMSPEPNCNRILEALDGFNLTMSYRSDSIDFTPYGWLEPWSGOAPHPPL 197
||| ||| :|:||||| :|:||||| :|:||||| :|
Qy 181 EVPSKEKLVCVVGVSNWPNEHARVKYYNELSKSIBIHTYGAFGFYVNDKNLIPTISTCKF 240
:||| ||| ||||| :|:||||| :|:||||| :|:||||| :|
Db 198 NLSAKTELVAWAVSNWKPKDPSARVRYYSLOAHLKVDVYGRSH-KPLPKGTMETLSRYKF 256
||| ||| :|:||||| :|:||||| :|:||||| :|
Qy 241 YLSFENSIIHKDYITEKLY-NAFLAGSPVLVGPRENVENIPADSIHVDFDNPSSELA 299
||| ||| :|:||||| :|:||||| :|:||||| :|
Db 257 YLAFENSLHPDIYTEKLWRNALEAWPVVGLGPSRSNYERFLPPDATIHVDDFQSFKDLA 316
||| ||| :|:||||| :|:||||| :|:||||| :|
Qy 300 KYLEVDKNNKKLYSYFNWRKDFTVNLR--FWESHACLACDHVKRHQEVKSVGNLSEKW 357
||| ||| :|:||||| :|:||||| :|:||||| :|
Db 317 RYLQELDORHDARYLSYFRWRET LR--PRFSWALAFCKACWLQESRYOTVRISAAWF 373
||| ||| :|:||||| :|:||||| :|:||||| :

RESULT 6

A45156

alpha-(1,3)-fucosyltransferase FUT6 - human

N:Alternate names: alpha-(1,3)-fucosyltransferase Fuc-TVI; fucosyltransferase 6; Lewi
C:Species: Homo sapiens (man)

C>Date: 26-May-1994 #sequence.revision 26-May-1994 #text_change 29-Sep-1999

C:Accession: A45156; JCI1228; I39050; I39051; I39052; I39053; I39054

R:Weston, B.W.; Smith, P.L.; Kelly, R.J.; Lowe, J.B.

J. Biol. Chem. 267, 24575-24584, 1992

A>Title: Molecular cloning of a fourth member of a human alpha(1,3)fucosyltransferase
l sialyl Lewis x epitopes.
A:Reference number: A45156; MUID:93077550

A:Accession: A45156

A:Molecule type: DNA

A:Residues: 1-359 <WES>

A:Cross-references: GB:I01698; NID:g182792; PIDN:AAB03078.1; PID:g1280210

R:Koszidin, K.L.; Bowen, B.R.

Biochem. Biophys. Res. Commun. 187, 152-157, 1992

A>Title: The cloning and expression of a human alpha-1,3 fucosyltransferase capable o
A:Reference number: JCI1228; MUID:92392318

A:Accession: JCI1228

A:Molecule type: mRNA

A:Residues: 1-359 <KOS>

A:Cross-references: GB:N98825; NID:g182491; PIDN:AAA99222.1; PID:g182492

A>Note: the authors translated the codon GAC for residue 219 as Asn

E:Cameron, H.S.; Szczepaniak, D.; Weston, B.W.

J. Biol. Chem. 270, 20112-20122, 1995

A>Title: Expression of human chromosome 19p alpha(1,3)-fucosyltransferase genes in no
A:Reference number: I39043; MUID:95378269

Db 173 PWSQPAHPPLNLSAKTELAVAWSNWGNPSARVRYQSLQAHKLVVDVYGRSH-KPLPQG 231
QY 230 NLPTISTCKFYLSFENSIIHKDYTEKLY-NAFLAGSVPPVVLGSPRSRENYENYIPADSFIIH 288
Db 232 TMMETLSRYKRYLAFENSLHPDYTEKLRWNALEAWAVPVVLGSPRSNRYERFLPPDAFIIH 291
QY 289 VEDFNSPSELAKYLKEVDKNNKLYLSFYFNWRKDFVTNLP--FWESHACIAC 338
Db 292 VDDFQSPDLARYLQELDKDHARYLSYFRWRETLR---PRFSWALAFCKAC 340
RESULT 9
A54057
alpha(1,3)-fucosyltransferase (EC 2.4.1.-) 7 precursor - human
N;Alternate names: leukocyte fucosyltransferase FucTVII
C;Species: Homo sapiens (man)
C;Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 20-Apr-2000
C;Accession: A54057; A53713
R;Sasaki, K.; Kurata, K.; Funayama, K.; Nagata, M.; Watanabe, E.; Ohta, S.; Hanai, N.; J. Biol. Chem. 269, 14730-14737, 1994
A;Title: Expression cloning of a novel alpha(1,3)-fucosyltransferase that is involved in B cell development
A;Reference number: A54057; MUID:94237894
A;Accession: A54057
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-342 <SAS>
A;Cross-references: GB:X78031; NID:g516292; PIDN:CAA54962.1; PID:g516293
R;Natsuka, S.; Gersten, K.M.; Zenita, K.; Kannagi, R.; Lowe, J.B. J. Biol. Chem. 269, 16789-16794, 1994
A;Title: Molecular cloning of a cDNA encoding a novel human leukocyte alpha-1,3-fucosyltransferase
A;Reference number: A53713; MUID:94266898
A;Accession: A53713
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-160,'A',163-303,'SV',306-342 <NAT>
A;Cross-references: GB:U08112; NID:g520463; PIDN:AAA56869.1; PID:g520464
C;Genetics:
A;Gene: GDB:FUT6
A;Cross-references: GDB:373982
A;Map position: 9pter-9qter
C;Superfamily: galactoside 3(4)-L-fucosyltransferase
C;Keywords: glycoprotein; glycosyltransferase; hexosyltransferase
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-342/Product: alpha(1,3)-fucosyltransferase 7 #status predicted <NAT>
F;81,291/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 31.6%; Score 622; DB 2; Length 342;
Best Local Similarity 43.3%; Pred. No. 1.5e-39;
Matches 130; Conservative 48; Mismatches 108; Indels 14; Gaps 8;
QY 65 TLVWVWVFP-GQTFDLTS--CQAMFNIGCHLTDRSLYNKSHAVLIHHRDISWDLTNLP 121
Db 48 TLVWVWVFPDQPELPSDTC-TRYGIARCHLSANRSLASADAVVPHRELQTRRSHLP 106
QY 122 QOARPPQKWIWNWLNLESPTTPQKSGIEHLFNLTLYRRSDIQVPGFLTVSTNPPVFE 181
Db 107 LAQRPQGPWWASMSPSHGLSHLURGIFFNNVLSYRRSDIDIFVPYGRLEPHWGSP-P 165
QY 182 VPSEKLVVWVSNWNPPEHARVYKYNLSKSIETHTYQAFGEVNDKNLPTISTCKFY 241
Db 166 LPAKSRVAANVSNFQERQLRARLYRQLAPHLRVDVFGNRPCLASCIVPIVAQYRFY 225
QY 242 LSFENSTHKDYTEKLY-NAFLAGSVPPVVLGSPRSRENYENYIPADSFTHVEDFNSPSELAK 300
Db 226 LSFENSHQRDYITEKFRNALVACTVPVLGPPPRATVEAFVPADAFVHVDVDFGSARELAA 285
QY 301 YLKEVDKNNKLYLSFYFNWRKDFVTNLP--FWESHACIACD---HVKKRQEVKSGVNLKWF 357
Db 286 FL--TGMNESRYQRFQAWRDLRLVRLFTDRERFCAICDRYPLPRSQVYE---DLEGWF 340
RESULT 10

I39049
alpha(1,3) fucosyltransferase FUT6-related splice form II - human
C;Species: Homo sapiens (man)
C;Date: 01-Mar-1996 #sequence_revision 01-Mar-1996 #text_change 29-Sep-1999
C;Accession: I39049
R;Cameron, H.S.; Szczepaniak, D.; Weston, B.W. J. Biol. Chem. 270, 20112-20122, 1995
A;Title: Expression of human chromosome 19p alpha(1,3)-fucosyltransferase genes in no
A;Reference number: I39043; MUID:95378269
A;Accession: I39049
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-304 <RES>
A;Cross-references: EMBL:U27332; NID:g967200; PIDN:AAC50191.1; PID:g967201
C;Genetics:
A;Gene: GDB:FUT6
A;Cross-references: GDB:135180; OMIM:136836
A;Map position: 19p13.3-19p13.3
C;Superfamily: galactoside 3(4)-L-fucosyltransferase
C;Keywords: alternative splicing
Query Match 24.3%; Score 478.5; DB 2; Length 304;
Best Local Similarity 43.0%; Pred. No. 9e-29;
Matches 98; Conservative 42; Mismatches 81; Indels 7; Gaps 6;
QY 55 STKTDYFNETTILVWVWVFPQTFDLTSCQAMF-NIQCHLTDRSLYNKSHAVLIHHRDI 113
Db 53 STGTGAHSPIILLTWTWPFNKPIALPRCSEMPGTADCNITADRKVYPQADAVIVHREV 112
QY 114 SWD-LTNLPOQARPPQKWIWNWLNLESPTTPQKSGIEHLFNLTLYRRSDIQVPGFLT 172
Db 113 MYNPSAQLPRSPRQQRWLFWSHESPCWQLKAMDGYFNLTMSYRSDSDIFTPTYGWLE 172
QY 173 V-STNPPF--VFEVPSKEKLVWVSNWNPPEHARVYKYNLSKSIETHTYQAFGEVYNDK 229
Db 173 PWSQPAHPPLNLSAKTELAVAWSNWGNPSARVRYQSLQAHKLVVDVYGRSH-KPLPQG 231
QY 230 NLPTISTCKFYLSFENSIIHKDYTEKLY-NAFLAGSVPPVVLGSPRSREN 276
Db 232 TMMETLSRYKRYLAFENSLHPDYTEKLRWNALEAWAVPVVLGSPSRN 279
RESULT 11
TL3270
hypothetical protein F59E12.13 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Mar-2000
C;Accession: T15270
R;Johnson, D.
Submitted to the EMBL Data Library, May 1997
A;Description: The sequence of C. elegans cosmid F59E12.
A;Reference number: Z18318
A;Accession: T15270
A;Molecule type: DNA
A;Residues: 1-414 <OJH>
A;Cross-references: EMBL:AF003386; NID:g2088833; PID:g2088845; PIDN:AAB54261.1; GSPDE
A;Experimental source: strain Bristol N2; clone F59E12
C;Genetics:
A;Gene: CESP:F59E12.13
A;Map position: 2
A;Introns: 90/3; 237/2; 279/3; 309/2; 339/2; 388/3
C;Superfamily: galactoside 3(4)-L-fucosyltransferase
Query Match 15.6%; Score 307; DB 2; Length 414;
Best Local Similarity 27.7%; Pred. No. 1.2e-15;
Matches 97; Conservative 59; Mismatches 120; Indels 74; Gaps 17;
QY 66 ILVWVWVFPQTFD---LTSCQAMFNIGCHLTDRSLYNKSHAVLIHHRDISWDLTNLP- 121
Db 67 ILYWTTTFGATVPSTALSDCPGL--TDRCVIDTNRHQLDSADAVVFAADIS----KFPL 120
QY 122 QOARPPQKWIWNWLNLESPTTPQKSG-----IEHLFNLTLYRRSD 163

Db 121 PVSRKPDQIEVFNSME-----TPNSGRFAVPGFKINVLNKNKPIYLDGFENWITSLYSSD 176
QY 164 IOVPYGFLLTVST---NPFVFEVPS-----KEKLVCVWVSNWNNPEHARVKKYNNLS 210
Db 177 AIHKGFFLIPTQIAESRGEKQVQYVQPKRLVKTMKGIFGLISNCHTKSKRELALQELG 236
QY 211 KSEIHTYGAQGEYVND---KNLIPTISTC-----KFYLSFENSIIKDYITEKLYNA 260
Db 237 KHLNV-TIG---GKCSDDRLKSLCICPAGVBCIDVFQYPPYIAIENTVCNDVYVTEKIWSR 292
QY 261 FLAGSPVVLGPRENYENYIPADSETHVDFENSPSELAKEYLKEVDKNNKLYLSVFNWR- 319
Db 293 ITVPSIPVW---RRVYQNTLPPKSEITAMDDYKNPSEMANHLEANSSTAYGEYFEWQ 350
QY 320 KDFTVNLPREWESHA-----CLACDHVKRHE-----YKSVGNLEKWFVN 359
Db 351 KGLWTSAP--WNAPGYRNGLCRCELLWAKAKDNETEVYKSYDNIWKWFON 398
RESULT 12
T16799
hypothetical protein T05A7.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T16799
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid T05A7.
A:Reference number: Z18580
A:Accession: T16799
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1652 <CHI>
A:Cross-references: EMBL:U40028; NID:g1055143; PID:g1055144; PIDN:AAA81114.1; CESP:T05A7
A:Gene: CESP.T05A7.5
A:Introns: 7/1; 43/3; 71/3; 132/1; 203/2; 247/3; 290/2; 315/3; 351/3; 407/2; 449/1; 504/
4/1; 1535/3; 1565/2; 1609/3
Query Match 15.4%; Score 304; DB 2; Length 1652;
Best Local Similarity 30.9%; Pred. No. 1.4e-14;
Matches 81; Conservative 54; Mismatches 103; Indels 24; Gaps 11;
QY 79 LPSCQMFNIQCHLTDRSLYNKSHAVLIHHRDI--SWDLTNLPQARPPPKWIMMNL 136
Db 1396 LATCPDVQNY--CRITQSESEFNADAVLFHNDYRGSTDFKMKRSORKGVPVYVLSL 1453
QY 137 ESHTPQKSGIEHLENLTIYRRSDIOVPYGFLLTVSTNPFVEV-----PSKEKLVGV 192
Db 1454 ESHTNMFRPD--SHMINWITRTDSWVAPYGTIVKLKNPVEDVNLAIWBGKTKTATWL 1512
QY 193 VSNWNPHEARVKKYNE-LSKSTIEHTYGAQGEYV-----NDKN--LIPTISTCKPYL 242
Db 1513 ASNCITONHRFDLIKKIIDNGFEIDWNC-GRQVSCAGVDNDESPCVLELIPKPYFI 1571
QY 243 SPENSITHDYTEKLYNAFL-AGSPVVLGPRENYENY-IPADSFHVEFNPSSELA 300
Db 1572 SMENSCNDYVTEKFWKALNDWMTPIVL--ARKYKIDGLVSDSAITAVDDYATLDEFLA 1629
QY 301 YLKEVDKNNKLYLSVFNWRKDF 322
Db 1630 HVKKVKNKEKDLFLSYHQWKEW 1651
RESULT 13
T23491
hypothetical protein K08F8.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T23491
R: Smye, R.
submitted to the EMBL Data Library, October 1995

A:Reference number: Z19747
A:Accession: T23491
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-451 <WLL>
A:Cross-references: EMBL:Z66497; PIDN:CAA91285.1; GSPDB:GN00020; CESP:K08F8.3
A:Experimental source: clone K08F8
C:Genetics:
A:Gene: CESP.K08F8.3
A:Map position: 2
A:Introns: 30/2; 53/3; 133/1; 195/3; 242/3; 277/3; 307/2; 342/3; 382/2
Query Match 14.5%; Score 285.5; DB 2; Length 451;
Best Local Similarity 30.4%; Pred. No. 5.9e-14;
Matches 87; Conservative 43; Mismatches 99; Indels 57; Gaps 12;
QY 67 LVWVWPFQOTDLTSCQMFNIQ-----CHLTDRSLYNKSHAVLIHHRDISWDLTNLP 121
Db 137 LILSNAGHSQD-----NLQCPDWNCEFTQVRAPADDAVLAHMDNF-----VP 184
QY 122 QOARPPQKWLWNNLESPTHTPOKSGIE-----HLFNLTIYRRSDIOVPYGFLL----- 171
Db 185 K-----PNQYVVYFQSESPAN-----SGIQRPDYINMILGRHDTAGSPYGVTKLGAK 236
QY 172 -----TVSTNPFVFEVPSKEKLVCVWVSNWNNPEHARVKKYNNLSKSTIEHTYGO----- 220
Db 237 SRKTQGVVDAN-----LVNGKAKGAAPVSHCQTNKREDFVKLQKHLQIDYIGCGCPMK 292
QY 221 -AFGEYVNDKNLIPTISTCKFYLSEFNSIHKDYITEKLYNAFLAGS--VPVVLGPRENYE 278
Db 293 CARGDSKCDTML--DIDYHFFVTFENSICEDYVTEKLVKSGYQNTIPIVL--KRLIVE 347
QY 279 NYIPADSFHVEFNPSSELAKEYLKEVDKNNKLYLSVFNWRKDFTV 324
Db 348 PFVPPNSFIAIDDPKSVKEMGDYLNLMNNKTAAYFEYFWRHDKV 393
RESULT 14
H96742
hypothetical protein F17M19.14 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: H96742
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chen, N.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Dewar, T.H.; Dwar,
ansen, C.W.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosomes 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: H96742
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-393 <STO>
A:Cross-references: GB:AE005173; NID:g6978923; PIDN:AAF34315.1; GSPDB:GN00141
A:Gene: F17M19.14
A:Map position: 1
Query Match 11.5%; Score 227.5; DB 2; Length 393;
Best Local Similarity 26.5%; Pred. No. 1.2e-09;
Matches 91; Conservative 46; Mismatches 129; Indels 77; Gaps 14;
QY 39 SPMESASSVLKMKNFSTKDYFNETILV--WVWPGTDFLTSCQMFNIQGHILTD 96
Db 82 SLOFCGCKLKKMH-----VKVLVKGWTWIPDNLNLSYCR-----CGMT-- 121
QY 97 RSLYNKSHAVLIHHRDISWDLTNLPQARPPPKWIMNLESPTHTPOKSGIEHFNLT 156


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Db 122 -CLWTKSSVLADSPDALLPETTPPLQRRVGDPLRVYMELEAGR---KRSREDIF--I 174
QY 157 TYRDSIQVPYCFGLVSNPFVFPVK--EKLVCWVSNWNPEHARVYKYNELSKS-- 212
Db 175 SYHAKDDVQTTYAGSLFHNNRNHYHISPHKNNVDVLVYSSSRCLPHRDR-----LAKSL 228
QY 213 --IEIHTYGA-----FGEYNDKN-----LIPTISTCKFYLSFENSIH 249
Db 229 DLIPHSFGKCLNNVGLDSALSMPYECVAEHAENAKWTDHLHCAMSHYKFVLAIENTAV 288
QY 250 KYITEKLYNAPLAGSVVVLGSPRENYENIPADSFIVHEDFNSPSELAKYLKEVDKNN 309
Db 289 ESYVTEKLFYALDGSVPYIFGAS--NVQDFVPPHVIDGSKFGSMQELAAAYVKRLGDDP 346
QY 310 KLYLSYFNWR-----KDFVNLPRFWESHACIACDHVKR 343
Db 347 VAYSEYHAMRRCLMGNYGKTRAVSL-----DTLPCRICEISR 385

RESULT 15
F96533
Probable fucosyltransferase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: F96533
R:Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: F96533
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-513 <STO>
A:Cross-references: GB:AE005173; NID:g10120428; PIDN:AAG13053.1; GSPDB:GN00141
C:Genetics:
A:Gene: F14J22.8
A:Map position: 1

Query Match 10.4%; Score 204.5; DB 2; Length 513;
Best Local Similarity 25.7%; Pred. No. 9.2e-08;
Matches 77; Conservative 50; Mismatches 122; Indels 51; Gaps 15;

QY 56 TKTDYFNEITILVWVPFGQTFDLTSCQ---AMFNIGQCH---LTTDRSLYNKSHA--V 106
Db 70 TLTDFFTQSPSL-----SQSPPARSDRKKIGLFTDRSCCEWLMREDSVTYSRDFTKDPI 123
QY 107 LIH--HRDISW---DLT-----NLPOQA---RPPFKWIWNLESPTHPTOKSGIEHL 151
Db 124 FISGGEKDFQWCVDCVTFGDSSGKTDAAFGLGCKFGTGLSIIRSMESAQYYPEN----- 177
QY 152 FNLTLTYRDSOI-----QVYGFVAVSTNPFVFEY-PSKEKLVCVW-VSNWNPEHA 201
Db 178 -DLAQARRRGYDIVMTSLSSDVPVGYFSWAEYDINSVPQKTERAIAAFAISNCGARNF 236
QY 202 RVKYYNELSK-STEIHTYGAFGAEYNDKNLIPTISTCKFYLSFENSIHKDYITEKLYNA 260
Db 237 RLQALPALMKTNIKIDSYGGCHNRDGVKDVKVEALKRYKFSLAFENTNEEDYVTEKFFQS 296
QY 261 FLAGSPVVLGSPRENYENIPA-DSFIHVEDFNSPSELAKYLKEVDKNNKLYLSYFNWR 319
Db 297 LVAGSPVVPVVGPP--PNIEEPAPASDSFLIKHTMEDVEPVAKRMKYLAANPAATYNQTLRWK 354
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Search completed: October 8, 2002, 16:54:35
Job time : 18.5 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 8, 2002, 15:06:57 ; Search time 8.5 Seconds
(without alignments)
1635,332 Million cell updates/sec

Title: US-09-744-748-1
Perfect score: 1970
Sequence: 1 MTSTSGILRPFLIVCIILG.....HVKRHOEYKSVGNLEKFWFN 359

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	706	35.8	433	1 FUT4_MOUSE	Q11127 mus musculus
2	694.5	35.3	433	1 FUT4_RAT	O62994 rattus norv
3	691.5	35.1	405	1 FUT4_HUMAN	P22083 homo sapien
4	670	34.0	361	1 FUT3_HUMAN	P21217 homo sapien
5	670	34.0	374	1 FUT5_HUMAN	Q11128 homo sapien
6	669	34.0	365	1 FUT3_BOVIN	Q11126 bos taurus
7	669	34.0	374	1 FUT5_PANTR	P56433 pan troglod
8	665.5	33.8	359	1 FUT6_HUMAN	P51993 homo sapien
9	663	33.7	372	1 FUT3_PANTR	O19058 pan troglod
10	662.5	33.6	359	1 FUT6_PANTR	P56434 pan troglod
11	622	31.6	342	1 FUT7_HUMAN	Q11130 homo sapien
12	582	29.5	389	1 FUT7_MOUSE	Q11131 mus musculus
13	356	18.1	503	1 FUT4_DROME	O9vul9 drosophila
14	297.5	15.1	425	1 FUTC_DROME	P83088 drosophila
15	257.5	13.1	443	1 FUTB_DROME	O9v1c1 drosophila
16	227.5	11.5	401	1 FUT3_ARATH	Q9c843 arabidopsis
17	204.5	10.4	513	1 FU12_ARATH	Q9fx97 arabidopsis
18	200	10.2	501	1 FU11_ARATH	O91jki arabidopsis
19	105	5.3	537	1 UGT5_CABEL	O20086 caenorhabdi
20	102	5.2	2059	1 TEGU_HSV7J	P52362 human herpe
21	101	5.1	663	1 GRIA_BACCE	O85467 bacillus ce
22	100.5	5.1	638	1 Y153_HUMAN	Q14166 homo sapien
23	100	5.1	810	1 Z33A_HUMAN	Q06730 homo sapien
24	98.5	5.0	623	1 RPOC_GUITH	O78484 guillardia
25	96	4.9	566	1 GUNB_PABLA	P23550 paenibacill
26	96	4.9	1092	1 DHE2_YEAST	P33327 saccharomyc
27	95	4.8	1480	1 CFTR_HUMAN	P13569 homo sapien
28	94	4.8	678	1 GSHL_YEAST	P32477 saccharomyc
29	93.5	4.7	781	1 HELL_HSVSA	Q01014 herpesvirus
30	93.5	4.7	986	1 EP1B_STAEP	P30195 staphylococ
31	93	4.7	387	1 CEXY_CLOSR	P40942 clostridium
32	91.5	4.6	1147	1 NRDC_HUMAN	O43847 homo sapien
33	91.5	4.6	1173	1 NIFU_ENTAG	P19543 enterobacte

ALIGNMENTS

RESULT 1

FUT4_MOUSE

ID	FUT4_MOUSE	STANDARD;	PRT;	433 AA.
AC	Q11127;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	01-MAR-2002 (Rel. 41, Last annotation update)			
DE	Alpha-(1.3)-fucosyltransferase (EC 2.4.1.-) (Galactoside 3-L-fucosyltransferase) (Fucosyltransferase 4) (FUCT-IV).			
GN	FUT4 OR ELFT.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96027607; PubMed=7559635;			
RA	Gersten K.M., Natsuka S., Trinchera M., Petryniak B., Kelly R.J., Hiraiwa N., Jenkins N.A., Gilbert D.J., Copeland N.G., Lowe J.B.;			
RA	"Molecular cloning, expression, chromosomal assignment, and tissue-specific expression of a murine alpha-(1,3)-fucosyltransferase locus corresponding to the human ELAM-1 ligand fucosyl transferase.";			
RL	J. Biol. Chem. 270:25047-25056(1995).			
RN	[2]			
RP	SEQUENCE FROM N.A. (SHORT FORM).			
RC	STRAIN=129/SV; TISSUE=Liver;			
RX	MEDLINE=97037075; PubMed=8882722;			
RA	Ozawa M., Muramatsu T.;			
RT	"Molecular cloning and expression of a mouse alpha-1,3 fucosyltransferase gene that shows homology with the human alpha-1,3 fucosyltransferase IV gene.";			
RL	J. Biochem. 119:302-308(1996).			
CC	-1- FUNCTION: MAY CATALYSE ALPHA-1,3 GLYCOSIDIC LINKAGES INVOLVED IN THE EXPRESSION OF LEWIS X/SSEA-1 AND VIM-2 ANTIGENS.			
CC	-1- PATHWAY: GLYCOSYLATION.			
CC	-1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI.			
CC	-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.			
CC	-1- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN STOMACH AND COLON. IT ALSO EXPRESSED IN THE LUNG, TESTIS, UTERUS, SMALL INTESTINE AND TO A LESSER EXTENT IN SPLEEN, AND OVARY. PRESENT IN TRACE AMOUNTS IN BRAIN, THYMUS, HEART, SMOOTH MUSCLE, KIDNEY AND BONE MARROW. NOT FOUND IN LIVER, SALIVARY GLAND AND PANCREAS.			
CC	-1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 10.			
CC	-----			
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CC	-----			
DR	EMBL; U33457; AAC52269.1; -;			
DR	EMBL; D63380; BAA09697.1; -;			

P00788 streptococc
Q9xll2 thermotoga
P11997 drosophila
P57633 buchnera ap
O9rlb6 rickettsia
P20929 homo sapien
P58176 sulfolobus
P87207 candida alb
O9z2h1 mus musculu
P26201 bos taurus
Q9uul4 schizosacch
P45492 campylobact

٥

RP VARIANTS LE(-) ARG-20; SER-170 AND ALA-336.
 RX MEDLINE=94059082; PubMed=8240337;
 RA Nishihara S., Yazawa S., Iwasaki H., Nakazato M., Kudo T., Ando T.,
 RA Narimatsu H.;
 RT "Alpha (1,3/1,4)fucosyltransferase (FucT-III) gene is inactivated by
 RT a single amino acid substitution in Lewis histo-blood type negative
 RT individuals.";
 RL Biochem. Biophys. Res. Commun. 196:624-631(1993).
 RN [6]
 RP VARIANTS LE(-) ARG-20 AND SER-170.
 RX MEDLINE=94033579; PubMed=8219240;
 RA Koda Y., Kimura H., Mekada E.;
 RT "Analysis of Lewis fucosyltransferase genes from the human gastric
 RT mucosa of Lewis-positive and -negative individuals.";
 RL Blood 82:2915-2919(1993).
 RN [7]
 RP VARIANTS LE(-) ARG-20 AND LYS-356.
 RX MEDLINE=94342259; PubMed=8063716;
 RA Mollicone R., Reguigne I., Kelly R.J., Fletcher A., Watt J., Oriol R.;
 RA Chatfield S., Aziz A., Cameron H.S., Weston B.W., Lowe J.B., Oriol R.;
 RT "Molecular basis for Lewis alpha(1,3/1,4)-fucosyltransferase gene
 RT deficiency (FUT3) found in Lewis-negative Indonesian pedigrees.";
 RL J. Biol. Chem. 269:20987-20994(1994).
 RN [8]
 RP VARIANTS LE(-) LYS-356.
 RX MEDLINE=95050753; PubMed=7961897;
 RA Nishihara S., Narimatsu H., Iwasaki H., Yazawa S., Akamatsu S.,
 RA Ando T., Seno T., Narimatsu I.;
 RT "Molecular genetic analysis of the human Lewis histo-blood group
 RT system.";
 RL J. Biol. Chem. 269:29271-29278(1994).
 RN [9]
 RP VARIANTS LE(-) ARG-20; ARG-68; MET-105 AND LYS-356.
 RX MEDLINE=96243526; PubMed=8801770;
 RA Elmgren A., Boerjeson C., Svensson L., Rydberg L., Larson G.;
 RT "DNA sequencing and screening for point mutations in the human Lewis
 RT 'FUT3' gene enables molecular genotyping of the human Lewis blood
 RT group system.";
 RL Vox Sang. 70:97-103(1996).
 RN [10]
 RP VARIANTS LE(-) ARG-68 AND MET-105.
 RX MEDLINE=97413801; PubMed=9268337;
 RA Elmgren A., Mollicone R., Costache M., Boerjeson C., Oriol R.,
 RA Harrington J., Larson G.;
 RT "Significance of individual point mutations, T202C and C314T, in the
 RT human Lewis 'FUT3' gene for expression of Lewis antigens by the human
 RT alpha'1,3/1,4'-fucosyltransferase, Fuc-TIII.";
 RL J. Biol. Chem. 272:21994-21998(1997).
 RN [11]
 RP VARIANTS LE(+) K-102 AND A-124, AND VARIANTS LE(-) N-162; R-223 AND
 RP M-270.
 RX MEDLINE=98366989; PubMed=9703429;
 RA Pang H., Liu Y., Koda Y., Soejima M., Jia J., Schlaphoff T.,
 RA du Toit E.D., Kimura H.;
 RT "Five novel missense mutations of the Lewis gene 'FUT3' in African
 RT 'Xhosa' and Caucasian populations in South Africa.";
 RL Hum. Genet. 102:675-680(1998).
 CC -1- FUNCTION: MAY CATALYZE ALPHA-1,3 AND ALPHA-1,4 GLYCOSIDIC LINKAGES
 CC INVOLVED IN THE EXPRESSION OF VIM-2, LEWIS A, LEWIS B, STALYL
 CC LEWIS X AND LEWIS X/SSA-1 ANTIGENS, MAY BE INVOLVED IN BLOOD
 CC GROUP LEWIS DETERMINATION; LEWIS-POSITIVE (LE(+)) INDIVIDUALS
 CC HAVE AN ACTIVE ENZYME WHILE LEWIS-NEGATIVE (LE(-)) INDIVIDUALS
 CC HAVE AN INACTIVE ENZYME.
 CC -1- CATALYTIC ACTIVITY: GDP-L-FUCOSE + 1,3-BETA-D-GALACTOSYL-
 CC (ALPHA-1,4-L-FUCOSYL)-N-ACETYL-D-GLUCOSAMINYL-R = GDP + 1,3-BETA-D-GALACTOSYL-
 CC (ALPHA-1,4-L-FUCOSYL)-N-ACETYL-D-GLUCOSAMINYL-R.
 CC -1- PATHWAY: GLYCOSYLATION.
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
 CC FORM IN TRANS CISTERNAE OF GOLGI.
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN STOMACH, COLON, SMALL
 CC INTESTINE, LUNG AND KIDNEY AND TO A LESSER EXTENT IN SALIVARY
 CC GLAND, BLADDER, UTERUS AND LIVER.
 CC -1- MISCELLANEOUS: ALSO ACTS ON THE CORRESPONDING 1,4-GALACTOSYL

CC DERIVATIVE, FORMING 1,3-L-FUCOSYL LINKS.
 CC -1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 10.
 CC -----
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 CC -----
 CC EMBL: X53578; CAA37641.1; -
 DR EMBL: U27328; AAC50187.1; -
 DR EMBL: U27326; AAC50185.1; -
 DR EMBL: U27327; AAC50186.1; -
 DR EMBL: D89324; BAA13941.1; -
 DR EMBL: D89325; BAA13942.1; -
 DR EMBL: AF131913; AAD33514.1; -
 DR PIR: A36669; A36669.
 DR MIM: 111100; -
 DR InterPro: IPR001503; Glyco_transf_10.
 DR Pfam: PF00852; Glyco_transf_10; 1.
 KW transferase; Glycosyltransferase; Glycoprotein; Blood group antigen;
 KW Signal-anchor; Golgi stack; Polymorphism; Blood group antigen.
 FT DOMAIN 1 15
 FT TRANSMEM 16 34
 FT DOMAIN 35 361
 FT CARBOHYD 154 154
 FT CARBOHYD 185 185
 FT VARIANT 20 20
 FT VARIANT 68 68
 FT VARIANT 102 102
 FT VARIANT 105 105
 FT VARIANT 124 124
 FT VARIANT 162 162
 FT VARIANT 170 170
 FT VARIANT 223 223
 FT VARIANT 270 270
 FT VARIANT 336 336
 FT VARIANT 356 356
 FT SEQUENCE 361 AA; 42117 MW; BF4398044F19C284 CRC64;
 FT Query Match 34.08; Score 670; DB 1; Length 361;
 FT Best Local Similarity 43.48; Pred. No. 9.9e-43;
 FT Matches 132; Conservative 54; Mismatches 98; Indels 20; Gaps 9;
 QY 66 ILVWVWPGQFDLTSCQMF-NIQGCHLTDRSLYKSHAVLIHHRDISWDL-----TN 119
 DB 65 ILLTWTPGHPIPVALSRCSEMVPGTADCHITADRVKYPOADTVIVHH---WDIMSNPKSR 120
 QY 120 LPQARPPFPQKWIMNLESPTHTPKSGIEHLNLTLYTRDSDIQVPGFLTV-STNPF 178
 DB 121 LPPSPRQGRWIFNLEPPPCQHLALDRYFNLTSYRSDSDIFTYPGWLEPWSGQA 180
 QY 179 --VFEPVSKELVVCVWSNNWNPENHARVRYQSLQHLKVDVYGRSH-KPLPKGTMMETLS 236
 DB 181 HPPLNLSAKTELVAWVSNWKPDSARVRYQSLQHLKVDVYGRSH-KPLPKGTMMETLS 239
 QY 237 TCKFYLSFENSITKDYITEKLY-NAFLAGSVPVVLGFSRENYENYIPADSFHVEDENSP 295
 DB 240 RYKFYLAFENSLHPDYITEKLRNALNALEAWVPVVLGFSRSNRYERFLPPDAFIHVDQSP 299


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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X87810; CAA61079.1;
CC DR InterPro: IPR001503; Glyco_transf_10.
CC KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
CC Signal-anchor; Golgi stack.
CC FT DOMAIN 1 14 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 15 34 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
CC FT DOMAIN 35 365 LUMENAL, CATALYTIC (POTENTIAL).
CC FT CARBOHYD 100 100 N-LINKED (GLCNAC...) (PROBABLE).
CC FT CARBOHYD 158 158 N-LINKED (GLCNAC...) (PROBABLE).
CC FT CARBOHYD 189 189 N-LINKED (GLCNAC...) (PROBABLE).
CC SQ SEQUENCE 365 AA; 42654 MW; 18715A361B0025D3 CRC64;
Query Match 34.0%; Score 669; DB 1; Length 365;
Best Local Similarity 39.4%; Pred. No. 1.2e-42;
Matches 145; Conservative 66; Mismatches 115; Indels 42; Gaps 12;
QY 11 PELIVCIILG-CFMACLLI---YIKPTNSW-----FSPMESASSVLKMKNFSTKTDY 60
DB 18 PGLLLQLLALCFSSYLRMSQKPKPKPMVMVSELGAPSQATGSSAHLPLR----- 68
QY 61 FNETTIVWVWPGFTDITSCQAMP-NIQGCHLTDRSLYKNSHAVLIHHRDISW-DLT 118
DB 69 -----VLLTWPFNTVALPRCSEMVPGADCNITADSNVYPOADAVIVHHWDIMYNPSANLPPP 123
QY 119 NLPOQARPPFOKWIWNLESPTHTPKSGIEHLNLTLYRRSDSDIOPVYCYFL-----T 172
DB 124 QLPPSPRPQGWVWFMSPESSNCKLKDLDGYFNLTWSYRSDSDIFWPYCKWLEWPQSP 183
QY 173 VSTNPFVEVPSKEKLVGVVSNWNPENHARVYKYNLSKSIETHTYQAGFYVNDKNLI 232
DB 184 VET---LLNISAKTLVAVVSNWNTDSIRVOYKLLKPHLQVDVYGR-FHTPLPALMA 239
QY 233 PTISCKEVLPSNTHKDYTEKLY-NAFLAGSVVPVGLGSRNENYIPADSFHVED 291
DB 240 KQLSQYKYLAFENSLHEDYITEKLRKALQAVVGVVGLGSRVNYEQFLPKAFIHVED 299
QY 292 FNSPELAKYLEVDKNNKLYLYSNFNRKDFTVNLP--FWESHACIACDVKRHOEYKS 349
DB 300 FQSPKDLAQYLLALDKDYASYLYNIFRWRETLR---PRFSWALMFCACWKLOQEPRYQT 356
QY 350 VGNLEKWF 357
DB 357 VPSIASWF 364
RESULT 7
FUT5_PANTR
ID FUT5_PANTR STANDARD; PRT; 374 AA.
AC P56433;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Alpha-(1.3)-fucosyltransferase (EC 2.4.1.65) (Galactoside 3-L-
DE fucosyltransferase) (Fucosyltransferase 5) (FUCT-V).
GN FUT5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OX NCBI_Taxid=9598;
RN [1]
RX SEQUENCE FROM N.A. PubMed=9368041;
MEDLINE=98037800;

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RA Costache M., Apoil P.-A., Cailles A., Elmgren A., Larson G.,
RA Henry S., Blanchard A., Iordachescu D., Oriol R., Mollicone R.;
RL "Evolution of fucosyltransferase genes in vertebrates.";
RL J. Biol. Chem. 272:29721-29728(1997).
CC -1- FUNCTION: MAY CATALYZE ALPHA-1,3 GLYCOSIDIC LINKAGES INVOLVED IN
CC THE EXPRESSION OF VIM-2, LEWIS X/SSEA-1 AND STALKY LEMIS X
CC ANTIGENS (BY SIMILARITY).
CC CC CATALYTIC ACTIVITY: GDP-L-FUCOSE + 1,3-BETA-D-GALACTOSYL-
CC N-ACETYL-D-GLUCOSAMINYLR-R = GDP + 1,3-BETA-D-GALACTOSYL-
CC (ALPHA-1,4-L-FUCOSYL)-N-ACETYL-D-GLUCOSAMINYLR-R.
CC -1- PATHWAY: GLYCOSYLATION
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC FORM IN TRANS CISTERNAE OF GOLGI
CC -1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 10.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: Y14034; CAA74361.1;
CC DR InterPro: IPR001503; Glyco_transf_10.
CC KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
CC Signal-anchor; Golgi stack.
CC FT DOMAIN 1 15 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 16 34 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
CC FT DOMAIN 35 374 LUMENAL, CATALYTIC (POTENTIAL).
CC FT CARBOHYD 60 60 N-LINKED (GLCNAC...) (POTENTIAL).
CC FT CARBOHYD 105 105 N-LINKED (GLCNAC...) (POTENTIAL).
CC FT CARBOHYD 167 167 N-LINKED (GLCNAC...) (POTENTIAL).
CC FT CARBOHYD 198 198 N-LINKED (GLCNAC...) (POTENTIAL).
CC SQ SEQUENCE 374 AA; 43034 MW; 3F35DEE8A8F1A2E2 CRC64;
Query Match 34.0%; Score 669; DB 1; Length 374;
Best Local Similarity 43.3%; Pred. No. 1.2e-42;
Matches 130; Conservative 58; Mismatches 100; Indels 12; Gaps 7;
QY 66 ILVWVWPGFTDITSCQAMP-NIQGCHLTDRSLYKNSHAVLIHHRDISW-DLTNLPQQ 123
DB 78 ILLTWPFNTVALPRCSEMVPGADCNITADSNVYPOADAVIVHHWDIMYNPSANLPPP 137
QY 124 ARPPQKWIWNLESPTHTPKSGIEHLNLTLYRRSDSDIOPVYCYFLTVSTNPFV---F 180
DB 138 TRPQGRWVNFMSPESSNCKRHLADGYFNLTWSYRSDSDIFTTYGWLQPMWGGQVHPPL 197
QY 181 EVPSKEKLVGVVSNWNPENHARVYKYNLSKSIETHTYQAGFYVNDKNLIPTISCKF 240
DB 198 NLSAKTELVAWVSNWNPENHARVYKYNLSKSIETHTYQAGFYVNDKNLIPTISCKF 256
QY 241 YLSPENSITHKDYITEKLY-NAFLAGSVVPVGLGSRNENYIPADSFTHVEDNSPELA 299
DB 257 YLAFENSLHEDYITEKLRNLEAWAVPVVGLGSRNENYIPADSFTHVEDNSPELA 316
QY 300 KYLEVDKNNKLYLYSNFNRKDFTVNLP--FWESHACIACDVKRHOEYKSVGNLEKWF 357
DB 317 RYLQELDKHARYLYSYFWRRETLR---PRFSWALMFCACWKLOQESRYQTVSIAAWF 373
RESULT 8
FUT6_HUMAN
ID FUT6_HUMAN STANDARD; PRT; 359 AA.
AC P51993;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Alpha-(1.3)-fucosyltransferase (EC 2.4.1.65) (Galactoside 3-L-
DE fucosyltransferase) (Fucosyltransferase 6) (FUCT-VI).
GN FUT6 OR FCT3A.

```


OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP MEDLINE=94237669; PubMed=8207002;
 RX MEDLINE=94237669; PubMed=8207002;
 RA Natsuka S., Gersten K.M., Zenita K., Kannagi R., Lowe J.B.;
 RT "Molecular cloning of a cDNA encoding a novel human leukocyte
 alpha-1,3-fucosyltransferase capable of synthesizing the sialyl
 Lewis x determinant.";
 RT J. Biol. Chem. 269:16789-16794(1994).
 RN [2]
 RP REVISIONS.
 RX MEDLINE=94337669; PubMed=8051184;
 RA Natsuka S., Gersten K.M., Zenita K., Kannagi R., Lowe J.B.;
 RT "Molecular cloning of a cDNA encoding a novel human leukocyte
 alpha-1,3-fucosyltransferase capable of synthesizing the sialyl
 Lewis x determinant.";
 RT J. Biol. Chem. 269:20806-20806(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94237894; PubMed=8182079;
 RA Sasaki K., Kurata K., Funayama K., Nagata M., Watanabe E., Ohta S.,
 RA Hanai N., Nishi T.;
 RT "Expression cloning of a novel alpha 1,3-fucosyltransferase that is
 involved in biosynthesis of the sialyl Lewis x carbohydrate
 determinants in leukocytes.";
 RT J. Biol. Chem. 269:14730-14737(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Hiraawa N., Hiraawa M., Kannagi R.;
 RT "The human selectin-ligand synthase (hFuc-T VII) gene structure and
 characterization of the promoter.";
 RT Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: MAY CATALYZE ALPHA-1,3 GLYCOSIDIC LINKAGES INVOLVED IN
 THE EXPRESSION OF SIALYL LEWIS X ANTIGENS.
 CC -!- CATALYTIC ACTIVITY: GDP-L-FUCOSE + ALPHA-2,3-NEU-N-ACETYL-1,4-
 BETA-D-GALACTOSYL-N-ACETYL-D-GLUCOSAMINYL-R = GDP + ALPHA-2,3-
 NEU-N-ACETYL-1,4-BETA-D-GALACTOSYL-(ALPHA-1,3-L-FUCOSYL)-
 R.
 CC N-ACETYL-D-GLUCOSAMINYL-R.
 CC -!- PATHWAY: GLYCOSYLATION.
 CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
 FORM IN TRANS CISTERNAE OF GOLGI.
 CC -!- TISSUE SPECIFICITY: LEUKOCYTIC/MYELOID LINEAGE CELLS.
 CC -!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 10.
 CC -----
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 CC -----
 DR EMBL; X78031; CAA54962.1; -;
 DR EMBL; U11282; AAA20488.1; -;
 DR EMBL; U08112; AAA56869.1; -;
 DR EMBL; AB012668; BAA32819.1; -;
 DR MIM; 602030; -;
 DR InterPro; IPR001503; Glyco.transf_10.
 DR Pfam; PF00852; Glyco.transf_10; 1.
 KW Transferase; Glycosyltransferase; Transmembrane; Glycoprotein;
 FT Signal-anchor; Golgi stack.
 FT DOMAIN 1 14
 FT TRANSMEM 15 36 CYTOPLASMIC (POTENTIAL).
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT LUMENAL, CATALYTIC (POTENTIAL).
 FT CARBOHYD 37 342
 FT CARBOHYD 81
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 291
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 161 162 GP -> A (IN REF. 1; AAA56869).
 FT CONFLICT 304 305 RL -> SV (IN REF. 1; AAA56869).
 FT SEQUENCE 342 AA; 39238 MW; D31BFF90DD64DFAB CRC64;

Query Match 31.6%; Score 622; DB 1; Length 342;
 Best Local Similarity 43.3%; Pred. No. 3.4e-39;
 Matches 130; Conservative 48; Mismatches 108; Indels 14; Gaps 8;
 QY 65 TILVWVWPF-GQTFDLTS--CQMFNIQCGHLTDRSLYKSHAVLIHHRDISWDLNLP 121
 DB 48 TILVWVWPFDPQPPELPSDTC-TRYGIARHLISANRSLASADAVVHFHRELQTRRSHLP 106
 QY 122 QQARPPQKWMNLSPTHTPOKSGIEHLNLTLYRRDSDIQVPYGFGLTVSTNPVFE 181
 DB 107 LAQPRGCPVWVWASMESPSHTHGLSHLGFNWVLSVRRSDIFVPCRLPHWGPSP-P 165
 QY 182 VPSKEKLVCVVSNWNPENHARVYKYNELSKSIEHTYQGAQGEYVNDKNLPISTCKFY 241
 DB 166 LPKRSVAAWVSNFORQLRARLYQLAPHLRVDFVGRANRPLCASCILVPTVAQYRFY 225
 QY 242 LSPENSHTKDYITEKLY-NAFLAGSVVVLGSPRENYENIPADSFTHVDFEFPNSPLAK 300
 DB 226 LSPENSQHRDIYITEKFWRNALVAGTVPVVLGPPRATYFAFVADAFVHVDVFGSARELAA 285
 QY 301 YLKEVDKNNKLYSYFNWRKDFVNLPRFWESHACLACD---HVKKRQEKYKSGNLEKWF 357
 DB 286 FL-TGMNESRYQRFPAWRDLRLVFTDWRERCAICDRYPLRQSVYE---DLEGWF 340
 RESULT 12
 ID FUT7_MOUSE STANDARD; PRT; 389 AA.
 AC Q11131;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DE 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Alpha-(1,3)-fucosyltransferase (EC 2.4.1.-) (Galactoside 3-L-
 fucosyltransferase) (Fucosyltransferase 7) (FUCT-VII).
 GN FUT7
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NIH;
 RX MEDLINE=96215226; PubMed=8626519;
 RA Smith P.L., Gersten K.M., Petryniak B., Kelly R.J., Rogers C.,
 RA Natsuka Y., Alford J.A. III, Scheidegger E.P., Natsuka S., Lowe J.B.;
 RT "Expression of the alpha(1,3)fucosyltransferase Fuc-TVII in lymphoid
 aggregate high endothelial venules correlates with expression of L-
 selectin ligands.";
 RT J. Biol. Chem. 271:8250-8259(1996).
 CC -!- FUNCTION: MAY CATALYZE ALPHA-1,3 GLYCOSIDIC LINKAGES INVOLVED IN
 THE EXPRESSION OF SIALYL LEWIS X ANTIGENS.
 CC -!- CATALYTIC ACTIVITY: GDP-L-FUCOSE + ALPHA-2,3-NEU-N-ACETYL-1,4-
 BETA-D-GALACTOSYL-N-ACETYL-D-GLUCOSAMINYL-R = GDP + ALPHA-2,3-
 NEU-N-ACETYL-1,4-BETA-D-GALACTOSYL-(ALPHA-1,3-L-FUCOSYL)-
 R.
 CC N-ACETYL-D-GLUCOSAMINYL-R.
 CC -!- PATHWAY: GLYCOSYLATION.
 CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
 FORM IN TRANS CISTERNAE OF GOLGI.
 CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE
 PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG AND BONE MARROW AND
 TO A MUCH LESSER EXTENT IN SPLEEN, SALIVARY GLAND AND SKELETAL
 MUSCLE.
 CC -!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 10.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

Db 316 LFDALERTVIVPVEGGA--DYSRILPHSYVDANRNFMSVEGLAKYMKLVVADPDLYYSYF 373
QY 317 NWRKDFTNLPRFESHACACDHV-----KRHOEKSXVGNLEKFWFN 359
Db 374 WWRSHYRLT-----YSSPFCDLARLHDPSECHKTQFYH---DIQSWWFN 415

RESULT 15
ID FUTE_DROME
AC Q9VIC1; 2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Alpha-(1,3)-fucosyltransferase B (EC 2.4.1.-) (Galactoside 3-L-fucosyltransferase)
GN FUCTB or CG4435.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OX Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
[1]
SEQUENCE FROM N.A.
RC STRAIN=Canton-S;
RX MEDLINE=21359431; PubMed=11382750;
RA Fabini G., Freilinger A., Altmann F., Wilson I.B.H.;
RT Identification of core alpha1,3-fucosylated glycans and cloning of
RT the requisite fucosyltransferase cDNA from Drosophila melanogaster;
RT potential basis of the neural anti-horseradish peroxidase epitope.;
RL J. Biol. Chem. 276:28058-28067(2001).
RN [2]
PP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yang M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abriel J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ihegwam C.,
RA Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattie B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muszy D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."

RL Science 287:2185-2195(2000).
CC -1- PATHWAY: Glycosylation.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Membrane-bound
CC form in trans cisternae of golgi (By similarity).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AJ302046; CAC41642.1; -
DR EMBL; AF003624; AAF52773.1; -
DR FlyBase; FBgn0032117; FUCTB.
KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
KW Signal-anchor; Golgi stack.
FT DOMAIN 1 6
FT TRANSMEM 7 27
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT LUMENAL, CATALYTIC (POTENTIAL).
FT N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 278 443
FT CARBOHYD 436 436
FT CARBOHYD 439 439
FT CARBOHYD 214 214
FT CONFLICT 408 408
FT CONFLICT 416 416
FT CONFLICT 416 416
FT CONFLICT 416 416
SQ SEQUENCE 443 AA; 51756 MW; C8FDA3CD2BFE118 CRC64;
Query Match 13.1%; Score 257.5; DB 1; Length 443;
Best Local Similarity 28.2%; Pred. No. 5.1e-12;
Matches 96; Conservative 49; Mismatches 138; Indels 57; Gaps 15;
QY 51 KNFFSTKDYFNETTILVWVWPGGTFDLTSCQAMFNIOGCHLTDRSLYNNKSHAVLIHH 110
Db 27 ENLIYENIKFNSPVELVW-WSRDMSWNY-DVQRCQGIHTRITKRSPRPWARGVLYG 84
QY 111 RDISDLTLNLPQOARPPFOKWIWMNLESPTHTPKSGIEHL--FNLTLYTRDSDI---- 164
Db 85 SNIKTGDFLP---RNEHQIALLHEESPRNTPFVSNKEFLRHFHTFTFSRYSNLPTT 141
QY 165 -QVPYGLFVSTNPFV-FEVPSSK-----EKLVCVWVSNMNPENHARVYKYNELSKSTEIHT 217
Db 142 MYLPSGEALTSKDYVYTFDGSKYGYRPSVTVFLQSDCDTMSGREDYVKELMKHLPIDS 201
QY 218 YGQAF-----GEYVND---KNLIPTISTCKFVLSFENSIIKDYITEKLYNAFLAGS 265
Db 202 YGSCLNRLDPERQKDYLNLYSPELLRFLSEYKFMIAENAAACPDYITEKEFWRPLMGV 261
QY 266 VPVVLG-PSRENVENYIPAD-SFIHVEDNSPSELAKYLKVEYDKNNKLYLSV----FNWR 319
Db 262 IPIYFGSPITKWE---PNKSAIFVNDQFQALVEYLKADNKKLYNSYRQHKLNRR 318
QY 320 -----KDFTVNL-----PRFESHACACDHV 341
Db 319 NFISNKKLLHNLVTROYHIGDSSPGASLFEKFECAVCYHV 358
Search completed: October 8, 2002, 16:52:47
Job time : 10.5 secs


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Db 28 VCVLAAGLCTALITYACWGLPLPMA-SPTPS-----RPVGVLL 68
QY 69 WWPFGQTFDL-----TSCQAMFNIOGCHLTDRSLYNKSHAVLIHHRDI-----SW----- 115
Db 69 WWPFGGRDSAPRPPDCPLRFNISGCHLLDRASYGEAAVLFHRLDLVKGPPDPPPP 128
QY 116 -----DLTNLPQO-----ARPPFKWIMNLESPTHTP-QKSGIEHL 151
Db 129 GQIHAETAEVDLRLVDYEAAAAAALATSSPPPGQVRWMMNFESPSGLSLASNL 188
QY 152 FNLTLYRRSDIOVPYGLTVSTNPFVEFPS-----KEKLVGVVWVNNWPEHARV 203
Db 189 FNTLSYRADSDVFPYGLYPRSHP--GDPFSGLAPPLSRKQGLVAVVSHWDERQARV 246
QY 204 KYNELKSIEHTYGOAF-GEYVNDKNLPTISACKFYLSFENSIIHKDYITEKLY-NAF 261
Db 247 RYHQLSQHVTVDVFGRGPGQVPPEIGLLHTVARYKFLAFENSQHLDIYITEKLWRLN 306
QY 262 LAGSVVVLGSPRENYENIPADSFTHVEDYNSPSELAKYLKVEDKNNKLYLSYFNWRKD 321
Db 307 LAGAVPVVLGPDPRANYERFVPRGAFIHDVDFPSASSLASYLFLDRNPVARYRFFHWR 366
QY 322 FTVNLPFRWESHACLADCHVXHQEY-KSVGNLEKWF 357
Db 367 YAVHITSFDEWPCWCRVQAVQVRAGDRPKSIRNLASF 403

RESULT 2
US-08-393-246-8
; Sequence 8, Application US/08393246
; Patent No. 5595900
; GENERAL INFORMATION:
; APPLICANT: LOWE, JOHN B.
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
; TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
; TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
; TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/220,433
; FILING DATE: 30-MAR-1994
; APPLICATION NUMBER: US 07/914,281
; FILING DATE: 20-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavalleye, Jean-Paul M. P.
; REGISTRATION NUMBER: 31,451
; REFERENCE/DOCKET NUMBER: 2363-060-55
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 405 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
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; MOLECULE TYPE: protein
US-08-393-246-8
Query Match 34.9%; Score 687.5; DB 1; Length 405;
Best Local Similarity 38.5%; Pred. No. 3.4e-58;
Matches 153; Conservative 59; Mismatches 110; Indels 75; Gaps 14;

QY 15 VCIILGCFMAC--LITYI-----KPTNSWIFSPMESASSVLKMKNEFFSTKTDYFNETTILV 68
Db 28 VCVLAAGLCTALITYACWGLPLPMA-SPTPS-----RPVGVLL 68
QY 69 WWPFGQTFDL-----TSCQAMFNIOGCHLTDRSLYNKSHAVLIHHRDI-----SW----- 115
Db 69 WWPFGGRDSAPRPPDCPLRFNISGCHLLDRASYGEAAVLFHRLDLVKGPPDPPPP 128
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Db 129 GQIHAETAEVDLRLVDYEAAAAAALATSSPPPGQVRWMMNFESPSGLSLASNL 188
QY 152 FNLTLYRRSDIOVPYGLTVSTNPFVEFPS-----KEKLVGVVWVNNWPEHARV 203
Db 189 FNTLSYRADSDVFPYGLYPRSHP--GDPFSGLAPPLSRKQGLVAVVSHWDERQARV 246
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Db 247 RYHQLSQHVTVDVFGRGPGQVPPEIGLLHTVARYKFLAFENSQHLDIYITEKLWRLN 306
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Db 307 LAGAVPVVLGPDPRANYERFVPRGAFIHDVDFPSASSLASYLFLDRNPVARYRFFHWR 366
QY 322 FTVNLPFRWESHACLADCHVXHQEY-KSVGNLEKWF 357
Db 367 YAVHITSFDEWPCWCRVQAVQVRAGDRPKSIRNLASF 403

RESULT 3
US-08-525-058A-8
; Sequence 8, Application US/08525058A
; Patent No. 5770420
; GENERAL INFORMATION:
; APPLICANT: LOWE, JOHN B.
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
; TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
; TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
; TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavalleye, Jean-Paul M. P.
; REGISTRATION NUMBER: 31,451
; REFERENCE/DOCKET NUMBER: 2363-060-55
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 405 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,531
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/393,246
; FILING DATE:
; APPLICATION NUMBER: US 08/220,433
; FILING DATE:
; APPLICATION NUMBER: US 07/914,281
; FILING DATE: 20-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavalleye, Jean-Paul M. P.
; REGISTRATION NUMBER: 31,451
; REFERENCE/DOCKET NUMBER: 2363-060-55
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 405 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-09-042-531-8

Query Match 34.9%; Score 687.5; DB 4; Length 405;
Best Local Similarity 38.5%; Pred. No. 3.4e-58;
Matches 153; Conservative 59; Mismatches 110; Indels 75; Gaps 14;
QY 15 VCIIIGCFMAC--LLIYI-----KPTNSWIFSPMESASSVLKMKNFSTKTDYFNETHILV 68
Db 28 VCVLAAGLCTALITYACWGQLPLPWA-SPTPS-----RPGVGLL 68
QY 69 WYWPFGQTFDL---TSCQAMFIQCHLTDRSLNKSHAVLIHHRDI-----SW---- 115
Db 69 WNEPFGGRDSAPRPDPCLRNISGCRLLTDRASGGAQVLFHHRDLVKGPPDPWPPW 128
QY 116 -----DLTNLPQO-----ARPPFOKWIWNLESPTHTP-QKSGIEHL 151
Db 129 GIOHTAEVDLRLVDYEEAAAAEALATSSPRPQGVWVMNFPESHSPGLSLASNL 188
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Db 189 FNTLSYRADSDVFPYGYLYPRSHP--GDPPSGLAPPLSRKQGLVAVVSHWDERQARY 246
QY 204 KYTNELSKSIEIHTYQAF-GEYVNDKNLIPTISACKFYLSFENSIIHKDYITEKLY-NAF 261
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Db 307 LAGAVPVVLGPDRAHYERFVPRGAFIHYDDFPSSASSLASYLFLDRNPVAVRYRHFHWR 366
QY 322 FTYNLPRFWEHSHACLDHVKRHOEY-KSVGNLEKWF 357
Db 367 YAVHITSFWEPCWRCVQAVQVQAGDRPKSIRNLASWF 403

RESULT 6
US-08-483-151-4
; Sequence 4, Application US/08483151
; Patent No. 585752
; GENERAL INFORMATION:
; APPLICANT: Seed, Brian
; APPLICANT: Holger, Jan
; TITLE OF INVENTION: FUCOSYLTRANSFERASE GENES AND USES THEREOF
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street

; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,151
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Lech, Karen F.
; REGISTRATION NUMBER: 35,238
; REFERENCE/DOCKET NUMBER: 00786/278001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 405 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-483-151-4
Query Match 34.2%; Score 673.5; DB 2; Length 405;
Best Local Similarity 37.8%; Pred. No. 7.6e-57;
Matches 150; Conservative 61; Mismatches 111; Indels 75; Gaps 14;
QY 15 VCIIIGCFMAC--LLIYI-----KPTNSWIFSPMESASSVLKMKNFSTKTDYFNETHILV 68
Db 28 VCVLAAGLCTALITYACWGQLPLPWA-SPTPS-----RPGVGLL 68
QY 69 WYWPFGQTFDL---TSCQAMFIQCHLTDRSLNKSHAVLIHHRDI-----SW---- 115
Db 69 WNEPFGGAISAPRPDPCLRNISGCRLLTDRASGGAQVLFHHRDLVKGPPDPWPPW 128
QY 116 -----DLTNLPQO-----ARPPFOKWIWNLESPTHTP-QKSGIEHL 151
Db 129 GIOHTAEVDLRLVDYEEAAAAEALATSSPRPQGVWVMNFPESHSPGLSLASNL 188
QY 152 FNLTITRYRSDIQVPGYFLVSTNPFVFEVPS-----KEKLVGVVSNWNPEHARY 203
Db 189 FNTLSYRADSDVFPYGYLYPRSHP--GDPPSGLAPPLSRKQGLVAVVSHWDERQARY 246
QY 204 KYTNELSKSIEIHTYQAF-GEYVNDKNLIPTISACKFYLSFENSIIHKDYITEKLY-NAF 261
Db 247 RYTHQLSQHVTVDFGRGGPGQVPEIGLHTVARYKFLAFENSQHLDYITEKLWRNAL 306
QY 262 LAGSVPVVLGPSRENYENIIPADSFIVHEDYNPSSELAKEYLKEVDKNNKLYLSYFNWRKD 321
Db 307 LAGAVPVVLGPDRAHYERFVPRGAFIHYDDFPSSASSLASYLFLDRNPVAVRYRHFHWR 366
QY 322 FTYNLPRFWEHSHACLDHVKRHOEY-KSVGNLEKWF 357
Db 367 YAVHITSFWEPCWRCVQAVQVQAGDRPKSIRNLASWF 403

RESULT 7
PCP-US91-00899-6
; Sequence 6, Application PC/TUS9100899
; GENERAL INFORMATION:
; APPLICANT: Lowe, John B.
; TITLE OF INVENTION: Method and Products For the Synthesis of
; TITLE OF INVENTION: Oligosaccharide Structures on Glycoproteins, Glycolipids,
; TITLE OF INVENTION: or as Free Molecules, and For the Isolation of Cloned
; TITLE OF INVENTION: Genetic Sequences That Determine These Structures
; NUMBER OF SEQUENCES: 16

;; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
;; TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
;; TITLE OF INVENTION: GLYCOPOLYMER, OR AS FREE MOLECULES, AND FOR THE ISOLATION
;; TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
;; NUMBER OF SEQUENCES: 14
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
;; ADDRESSEE: P.C.
;; STREET: 1755 Jefferson Davis Highway, Fourth Floor
;; CITY: Arlington
;; STATE: Virginia
;; COUNTRY: U.S.A.
;; ZIP: 22202
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/393,246
;; FILING DATE:
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/220,433
;; FILING DATE: 30-MAR-1994
;; APPLICATION NUMBER: US 07/914,281
;; FILING DATE: 20-JUL-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lavalleye, Jean-Paul M. P.
;; REGISTRATION NUMBER: 31,451
;; REFERENCE/DOCKET NUMBER: 2363-060-55
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703)521-4500
;; TELEFAX: (703)486-2347
;; TELEX: 248855 OPAT UR
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 361 amino acids
;; TYPE: amino acid
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
US-08-393-246-2

Query Match 33.9%; Score 667; DB 1; Length 361;
Best Local Similarity 43.1%; Pred. No. 2.7e-56;
Matches 131; Conservative 55; Mismatches 98; Indels 20; Gaps 9;

QY 66 ILVWVPFGQTDLTSCQAMF-NIOGCHLTDRSLYNKSHAVLIHHRDISWDL-----TN 119
DB 65 ILLWTWPFHIPVALSRCSEMPGTADCHITADRKVYPOADTVIVHH---WDIMSNPKSR 120
QY 120 LPOQARPPFQKWIWMLESPTHTPQKSGIEHLNLTLYRRDSDIQVYGFGLTV-STNPF 178
DB 121 LPPSPRPOGORIWFNLEPPPCQHLALDRYFNLTMSYRSDSDIFTFYGWLSPWQCPA 180
QY 179 --VFEPVPSKEKLVGVVSNWNPENHARVKYNNELSKSIEHTIYQOAFGEVNDKNLIPTIS 236
DB 181 HPPLNLSAKTELVAWAVSNWPKDSARVRYQSLQAHKLVVDYVGRSH-KPLPKGTMMETLS 239
QY 237 ACKFYLSFENSIIHKDYITEKLY-NAFLAGSVVVLGSPSRNENYIPADSFHVEDYNSP 295
DB 240 RYKFYLAENSIIHKDYITEKLY-NAFLAGSVVVLGSPSRNENYIPADSFHVEDYNSP 299
QY 296 SELAKLYKEVDKNKLYLSYNWRKDFVNLPR--FWSHACACLDHVKRQEKYSYGNL 353
DB 300 KDLARYLQELQKHARYLSYFRWRRTLR---PRFSWALDFCKACWKLOQESRYQTVRSI 356
QY 354 EKWF 357
DB 357 AAWF 360
RESULT 10

US-08-273-411-3
;; Sequence 3, Application US/08273411
;; Patent No. 5625124
;; GENERAL INFORMATION:
;; APPLICANT: Falk, Per
;; APPLICANT: Gordon, Jeffrey I.
;; TITLE OF INVENTION: Animal Model for Gastro-Intestinal
;; TITLE OF INVENTION: Disease
;; NUMBER OF SEQUENCES: 10
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Patrea L. Pabst
;; STREET: 1100 Peachtree Street, Suite 2800
;; CITY: Atlanta
;; STATE: Georgia
;; COUNTRY: USA
;; ZIP: 30309-4530
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/273,411
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Pabst, Patrea L.
;; REGISTRATION NUMBER: 31,284
;; REFERENCE/DOCKET NUMBER: WU106
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (404) 815-6508
;; TELEFAX: (404) 815-6555
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 361 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: Internal
;; FEATURE:
;; NAME/KEY: misc-feature
;; LOCATION: 1-361
;; OTHER INFORMATION: /note= "GDP-L-fucose:beta-D-N-acetylglucosaminide-3,4-alp
;; PUBLICATION INFORMATION:
;; AUTHORS: Kukowska-Latallo, et al.
;; JOURNAL: Genes & Development
;; VOLUME: 4
;; PAGES: 1288-1303
;; DATE: 1990
;; RELEVANT RESIDUES IN SEQ ID NO: 3: FROM 1 TO 361
US-08-273-411-3

Query Match 33.9%; Score 667; DB 1; Length 361;
Best Local Similarity 43.1%; Pred. No. 2.7e-56;
Matches 131; Conservative 55; Mismatches 98; Indels 20; Gaps 9;
QY 66 ILVWVPFGQTDLTSCQAMF-NIOGCHLTDRSLYNKSHAVLIHHRDISWDL-----TN 119
DB 65 ILLWTWPFHIPVALSRCSEMPGTADCHITADRKVYPOADTVIVHH---WDIMSNPKSR 120
QY 120 LPOQARPPFQKWIWMLESPTHTPQKSGIEHLNLTLYRRDSDIQVYGFGLTV-STNPF 178
DB 121 LPPSPRPOGORIWFNLEPPPCQHLALDRYFNLTMSYRSDSDIFTFYGWLSPWQCPA 180
QY 179 --VFEPVPSKEKLVGVVSNWNPENHARVKYNNELSKSIEHTIYQOAFGEVNDKNLIPTIS 236
DB 181 HPPLNLSAKTELVAWAVSNWPKDSARVRYQSLQAHKLVVDYVGRSH-KPLPKGTMMETLS 239
QY 237 ACKFYLSFENSIIHKDYITEKLY-NAFLAGSVVVLGSPSRNENYIPADSFHVEDYNSP 295
DB 300 KDLARYLQELQKHARYLSYFRWRRTLR---PRFSWALDFCKACWKLOQESRYQTVRSI 356
QY 354 EKWF 357
DB 357 AAWF 360
RESULT 10


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QY 179 --VEVPSKEKLVGVVSNMNNPEHARVYKYNELSKSIEIHTYGOAFGEYVNDKNLIPTIS 236
DB 181 HPPLNLSAKTELAVAWVSNMKNPDSARVYQSLQHLKVDVYGRSH-KPLPKGTMMETLS 239
QY 237 ACKFYLSPENSIRKDYITEKLY-NAFLAGSVVVLGSPSRENYENYIPADSFIVHEDYNP 295
DB 240 RYKFLAFENSLHPDYITEKLRNLALEAWAVPVVLGSPSRSNYERFLPDAFIVDDFQSP 299
QY 296 SELAKYLEVDKNKLYSYFNWRKDFTVNLPR--FWESHACIACDHBVKKRHOEYKSVGNL 353
DB 300 KDLARYLQELDKDHARYLSYFWRRETLR---PRSFNWALDFCKACWKLOQESRYQTVRSI 356
QY 354 EKWF 357
DB 357 AAWF 360

RESULT 13
US-09-042-531-2
; Sequence 2, Application US/09042531
; Patent No. 6268193
; GENERAL INFORMATION:
; APPLICANT: LOWE, JOHN B.
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
; OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
; TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
; OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,531
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/393,246
; FILING DATE:
; APPLICATION NUMBER: US 08/220,433
; FILING DATE: 30-MAR-1994
; APPLICATION NUMBER: US 07/914,281
; FILING DATE: 20-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavalleye, Jean-Paul M. P.
; REGISTRATION NUMBER: 31,451
; REFERENCE/DOCKET NUMBER: 2363-060-55
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-09-042-531-2

Query Match 33.9%; Score 667; DB 4; Length 361;
Best Local Similarity 43.1%; Pred. No. 2.7e-56;
Matches 131; Conservative 55; Mismatches 98; Indels 20; Gaps 9;
QY 66 ILVWVWPFQFDLTSCQAMP-NIOGCHLTTRSLYKNSHAVLIHRRDISWDL-----TN 119
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DB 65 ILLWTWPHIPVALSRCSEMPVPGTADCHITADRKVYPOADTVIVHH-----WDIMSNPKSR 120
QY 120 LPQOARPPFQKWMNLESPTHTPOKSGIEHLFNLTLYRRDSIQVYGLTV-STNPF 178
DB 121 LPPSPRQOQRIWENLEPPPCQHLQALDRYFNLTMSYRSDSDIFTYPYGWLEPWSGPA 180
QY 179 --VEVPSKEKLVGVVSNMNNPEHARVYKYNELSKSIEIHTYGOAFGEYVNDKNLIPTIS 236
DB 181 HPPLNLSAKTELAVAWVSNMKNPDSARVYQSLQHLKVDVYGRSH-KPLPKGTMMETLS 239
QY 237 ACKFYLSPENSIRKDYITEKLY-NAFLAGSVVVLGSPSRENYENYIPADSFIVHEDYNP 295
DB 240 RYKFLAFENSLHPDYITEKLRNLALEAWAVPVVLGSPSRSNYERFLPDAFIVDDFQSP 299
QY 296 SELAKYLEVDKNKLYSYFNWRKDFTVNLPR--FWESHACIACDHBVKKRHOEYKSVGNL 353
DB 300 KDLARYLQELDKDHARYLSYFWRRETLR---PRSFNWALDFCKACWKLOQESRYQTVRSI 356
QY 354 EKWF 357
DB 357 AAWF 360

RESULT 14
PCT-US91-00899-7
; Sequence 7, Application PC/TUS9100899
; GENERAL INFORMATION:
; APPLICANT: Lowe, John B.
; TITLE OF INVENTION: Method and Products For the Synthesis of
; OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS, GLYCOLIPIDS,
; OR AS FREE MOLECULES, AND FOR THE ISOLATION OF CLONED
; GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/00899
; FILING DATE: 19910214
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavalleye Ph.D., Jean-Paul
; REGISTRATION NUMBER: 31,451
; REFERENCE/DOCKET NUMBER: 2363-021-55 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-5940
; TELEFAX: (703)486-2347
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: Blood
; CELL LINE: A431
; PCT-US91-00899-7

Query Match 33.9%; Score 667; DB 5; Length 361;
Best Local Similarity 43.1%; Pred. No. 2.7e-56;
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Matches 131; Conservative 55; Mismatches 98; Indels 20; Gaps 9;
Qy 66 ILVWVWPGQTFDLTSQAMF-NIQGCHLTDRSLYKSHAVLIHHRDISWDL-----TN 119
Db 65 ILLWTWPFHIPVALSRGSEMPVGTADCHITADRVYPOADTVIVHH-----WDIMSNPKSR 120
Qy 120 LPOARPPFQKWIWNLESPTHTPKSGIEHLFNLTLTYRSDIOVPYGLTV-STNPF 178
Db 121 LPPSRPQGWIMFNLEPPNCHLEALDRYFNLMTSYRSDSDIFTYPGWLEPWSGQA 180
Qy 179 --VEVPSKEKLVCVVSNWNPENPEHARVYKYNELSKSIEIHTYGOAFGEVYVNDKNLIPTIS 236
Db 181 HPLNLSAKTELVAWAVSNWKPDSARVYQSLQAHKVDVYGRSH-KPLPKGTMMETLS 239
Qy 237 ACKYLFSENSIHKDYITEKLY-NAFLAGSVVVLGSPSRENYENIYPADSFHVEDYN 295
Db 240 RYKFLAPENSILHPDYITEKLRNALALEAWAVPVVLGSPSRNYERFLPPDAFIHVD 299
Qy 296 SELAKYLEVDKNNKLYLSYFNWRKDFTVNLP--FWESHACLADCHVKRHOEYKSVGNL 353
Db 300 KDLARYQLQELDKHARYLSYFRWRETLR---PRSFNALDFCKACWKLOQESRYQTVRSI 356
Qy 354 EKWF 357
Db 357 AAWF 360

RESULT 15
US-07-914-281-11
; Sequence 11, Application US/07914281
; Patent No. 5324663
; GENERAL INFORMATION:
; APPLICANT: LOWE, JOHN B.
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
; TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
; TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
; TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCU
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/914,281
; FILING DATE: 19920720
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavalleye, Jean-Paul M. P.
; REGISTRATION NUMBER: 31,451
; REFERENCE/DOCKET NUMBER: 2363-060-55
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-07-914-281-11
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Query Match 33.9%; Score 667; DB 1; Length 374;
Best Local Similarity 43.7%; Pred. No. 2.8e-56;

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Matches 131; Conservative 58; Mismatches 99; Indels 12; Gaps 8;
Qy 66 ILVWVWPGQTFDLTSQAMF-NIQGCHLTDRSLYKSHAVLIHHRDISWD-LTNLPQQ 123
Db 78 ILLWTWPFTEVALPRGSEMPVGAADCNITADSSVYPOADAVIVHHWDIMYNPSANLPPP 137
Qy 124 ARPPFQKWIWNLESPTHTPKSGIEHLFNLTLTYRSDIOVPYGLTV-STNPF--VF 180
Db 138 TRPOGQRWIMFMSGPSNCRHLEALDGYFNLMTSYRSDSDIFTYPGWLEPWSGQPAHPL 197
Qy 181 EVPSKEKLVCVVSNWNPENPEHARVYKYNELSKSIEIHTYGOAFGEVYVNDKNLIPTISACKF 240
Db 198 NLSAKTELVAWAVSNWKPDSARVYQSLQAHKVDVYGRSH-KPLPKGTMMETLSRYKF 256
Qy 241 YLSPENSIIHKDYITEKLY-NAFLAGSVVVLGSPSRENYENIYPADSFHVEDYN 299
Db 257 YLAFENSLHPDYITEKLRNALALEAWAVPVVLGSPSRNYERFLPPDAFIHVD 316
Qy 300 KYLKEVDKNNKLYLSYFNWRKDFTVNLP--FWESHACLADCHVKRHOEYKSVGNLEKWP 357
Db 317 RYLOELDKDHARYLSYFRWRETLR---PRSFNALDFCKACWKLOQESRYQTVRSIAAWF 373
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Search completed: October 8, 2002, 18:52:18
Job time : 20 secs

